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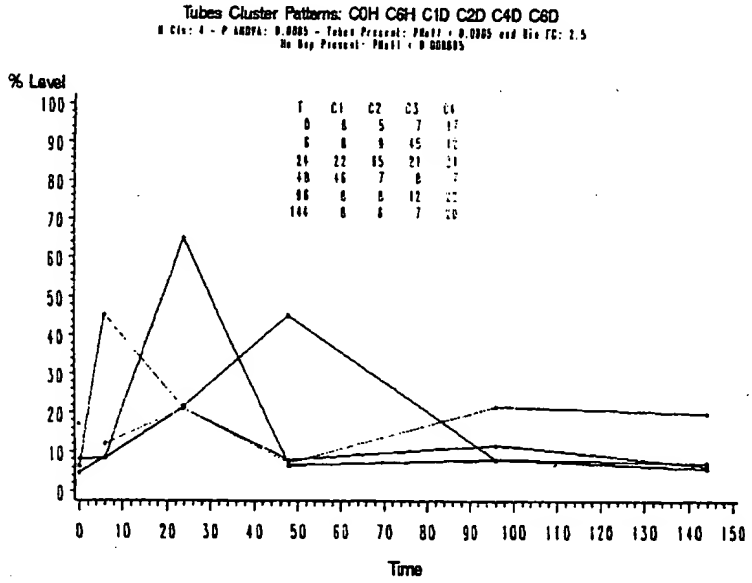

(57) Abstract: Described herein are methods that can be used for diagnosis of angiogenesis and angiogenic phenotypes. Also described herein are methods that can be used to screen candidate bioactive agents for the ability to modulate angiogenesis. Additionally, methods and molecular targets (genes and their products) for therapeutic intervention in disorders associated with angiogenesis are described.

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NOVEL METHODS OF DIAGNOSIS OF ANGIOGENESIS, COMPOSITIONS AND METHODS OF SCREENING FOR ANGIOGENESIS MODULATORS

FIELD OF THE INVENTION

The invention relates to the identification of expression profiles and the nucleic acids involved in angiogenesis, and to the use of such expression profiles and nucleic acids in diagnosis of angiogenesis. The invention further relates to methods for identifying candidate agents and/or targets which modulate angiogenesis.

BACKGROUND OF THE INVENTION

New blood vessel development comprises the formation of veins (vasculogenesis) and arteries (angiogenesis). Angiogenesis plays a normal role in embryonic development, as well as menstration, wound healing. Angiogenesis also plays a crucial pathogenic role in a variety of disease states, including cancer, proliferative diabetic retinopathy, and maintaining blood flow to chronic inflammatory sites.

Angiogenesis has a number of stages. The early stages of angiogenesis include endothelial cell protease production, migration of cells and proliferation. The early stages also appear to require some growth factors, with VEGF, TGF-α, angiostatin, and selected chemokines all putatively playing a role. Later stages of angiogenesis include the population of the vessels with mural cells (pericytes or smooth muscle cells), basement membrane production and the induction of vessel bed specializations. The final stages of vessel formation include what is known as "remodeling", wherein a forming vasculature becomes a stable, mature vessel bed.

Thus, understanding the genes, proteins and regulatory mechanisms that occur during angiogenesis would be desirable. Accordingly, it is an object of the invention to provide methods that can be used to screen candidate bioactive agents for the ability to modulate angiogenesis. Additionally, it is an object to provide molecular targets for therapeutic intervention in disease states which either have an undesirable excess or a deficit in angiogenesis.

SUMMARY OF THE INVENTION

The present invention provides novel methods for diagnosis and prognosis evaluation for angiogenesis, as well as methods for screening for compositions which modulate angiogenesis. Methods of treatment of disorders associated with angiogenesis, as well as compositions are also provided herein.

In one aspect, a method of screening drug candidates comprises providing a cell that expresses an expression profile gene or fragments thereof. or fragments thereof. Preferred embodiments of the expression profile gene are genes which are differentially expressed in angiogenesis cells, compared to other cells. Preferred embodiments of expression profile genes used in the methods herein include but are not limited to the group consisting of AAA4, AAA1, Edg-1, alpha 5 beta1 integrin, endomucin and matrix metalloproteinase 10; fragments of the proteins of this group are also preferred. It is understood that molecules for use in the present invention may be from any figure or any subset of listed molecules. Therefore, for example, any one or more of the genes listed above can be used in the methods herein. In another embodiment, a nucleic acid is selected from Tables 1, 2, 3, 4 or 5. Preferred nucleic acids are in Table 4, and most preferably Table 5. The method further includes adding a drug candidate to the cell and determining the effect of the drug candidate on the expression of the expression profile gene.

In one embodiment, the method of screening drug candidates includes comparing the level of expression in the absence of the drug candidate to the level of expression in the presence of the drug candidate, wherein the concentration of the drug candidate can vary when present, and wherein the comparison can occur after addition or removal of the drug candidate. In a preferred embodiment, the cell expresses at least two expression profile genes. The profile genes may show an increase or decrease.

Also provided herein is a method of screening for a bioactive agent capable of binding to an angiogenesis modulator protein (AMP), the method comprising combining the AMP and a candidate bioactive agent, and determining the binding of the candidate agent to the AMP. Preferably the AMP is a protein or fragment thereof selected from the group consisting of AAA4, AAA1, Edg-1, alpha 5 beta1 integrin, endomucin and matrix metalloproteinase 10. In another embodiment, the proteins is encoded by a nucleic acid selected from Tables 1, 2, 3, 4 or 5. Preferred nucleic acids are in Table 4, and most preferably Table 5.

Further provided herein is a method for screening for a bioactive agent capable of modulating the activity of an AMP. In one embodiment the method comprises combining the AMP and a candidate bioactive agent, and determining the effect of the candidate agent on the bioactivity of the AMP. Preferably the AMP is a protein or fragment thereof selected from the group consisting of AAA4, AAA1, Edg-1, alpha 5 beta1 integrin, endomucin and matrix metalloproteinase 10. In another embodiment, the proteins is encoded by a nucleic acid selected from Tables 1, 2, 3, 4 or 5. Preferred nucleic acids are in Table 4, and most preferably Table 5.

Also provided is a method of evaluating the effect of a candidate angiogenesis drug comprising administering the drug to a transgenic animal expressing or over-expressing the AMP, or an animal lacking the AMP, for example as a result of a gene knockout.

Additionally, provided herein is a method of evaluating the effect of a candidate angiogenesis drug comprising administering the drug to a patient and removing a cell sample from the patient. The expression profile of the cell is then determined. This method may further comprise comparing the expression profile to an expression profile of a healthy individual. In a preferred embodiment, the expression profile includes a gene of Table 1, Table 2, Table 3, Table 4 or Table 5.

Moreover, provided herein is a biochip comprising one or more nucleic acid segments which encode an angiogenesis protein, preferable selected from the group consisting of AAA4, AAA1, Edg-1, alpha 5 beta1 integrin, endomucin and matrix metalloproteinase , or fragment thereof, wherein the biochip comprises fewer than 1000 nucleic acid probes. Preferably at least two nucleic acid segments are included. In another embodiment, the nucleic acid selected from Tables 1, 2, 3, 4 or 5. Preferred nucleic acids are in Table 4, and most preferably Table 5.

Furthermore, a method of diagnosing a disorder associated with angiogenesis is provided. The method comprises determining the expression of a gene which encodes an angiogenesis protein preferable selected from the group consisting of AAA4, AAA1, Edg-1, alpha 5 beta1 integrin, endomucin and matrix metalloproteinase 10, or fragment thereof in a first tissue type of a first individual, and comparing the distribution to the expression of the gene from a second normal tissue type from the first individual or a second unaffected individual. In another embodiment, the proteins is encoded by a nucleic acid selected from Tables 1, 2, 3, 4 or 5. Preferred nucleic acids are in Table 4, and most preferably Table 5. A difference in the expression indicates that the first individual has a disorder associated with angiogenesis.

In another aspect, the present invention provides an antibody which specifically binds to an angiogenesis preferably selected from the group consisting of AAA4, AAA1, Edg-1, alpha 5 beta1 integrin, endomucin and matrix metalloproteinase 10 or fragment thereof. . In another embodiment, the proteins is encoded by a nucleic acid selected from Tables 1, 2, 3, 4 or 5. Preferred nucleic acids are in Table 4, and most preferably Table 5. In a preferred embodiment the fragment of AAA1 is selected from AAA1p1 or AAA1p2. Other preferred fragments for the angiogenesis proteins are shown in the figures.

In one embodiment a method for screening for a bioactive agent capable of interfering with the binding of a angiogenesis modulating protein (AMP) or a fragment thereof and an antibody which binds to said AMP or fragment thereof. In a preferred embodiment, the method comprises combining an AMP or fragment thereof, a candidate bioactive agent and an antibody which binds to said AMP or fragment thereof. The method further includes determining the binding of said AMP or fragment thereof and said antibody. Wherein there is a change in binding, an agent is identified as an interfering agent. The interfering agent can be an agonist or an antagonist. Preferably, the agent inhibits angiogenesis.

In a further aspect, a method for inhibiting angiogenesis is provided. In one embodiment, the method comprises administering to a cell a composition comprising an antibody to an angiogenesis modulating protein, preferably selected from the group consisting of AAA4, AAA1, Edg-1, alpha 5 beta1 integrin, endomucin and matrix metalloproteinase 10, or fragment thereof. In another embodiment, the proteins is encoded by a nucleic acid selected from Tables 1, 2, 3, 4 or 5. Preferred nucleic acids are in Table 4, and most preferably Table 5. The method can be performed in vitro or in vivo, preferably in vivo to an individual. In a preferred embodiment the method of inhibiting angiogenesis is provided to an individual with a disorder associated with angiogenesis such as cancer. As described herein, methods of inhibiting angiogenesis can be performed by administering an inhibitor of the activity of an angiogenesis protein, including an antisense molecule to the gene or its gene products, and preferable small molecules.

Also provided herein are methods of eliciting an immune response in an individual. In one embodiment a method provided herein comprises administering to an individual a composition comprising an angiogenesis modulating protein, preferably selected from the group consisting of AAA4, AAA1, Edg-1, alpha 5 beta1 integrin, endomucin and matrix metalloproteinase 10, or fragment thereof. In another embodiment, the proteins is encoded by a nucleic acid selected from Tables 1, 2, 3, 4 or 5. Preferred nucleic acids are in Table 4, and most preferably Table 5. In another aspect, said composition comprises a nucleic acid comprising a sequence encoding an angiogenesis modulating protein, preferably selected from the group consisting of AAA4, AAA1, Edg-1, alpha 5 beta1 integrin,

endomucin and matrix metalloproteinase 10, or fragment thereof. In another embodiment, the proteins is encoded by a nucleic acid selected from Tables 1, 2, 3, 4 or 5. Preferred nucleic acids are in Table 4, and most preferably Table 5.

Further provided herein are compositions capable of eliciting an immune response in an individual. In one embodiment, a composition provided herein comprises an angiogenesis modulating protein, preferably selected from the group consisting of AAA4, AAA1, Edg-1, alpha 5 beta1 integrin, endomucin and matrix metalloproteinase 10, or fragment thereof. In another embodiment, the proteins is encoded by a nucleic acid selected from Tables 1, 2, 3, 4 or 5. Preferred nucleic acids are in Table 4, and most preferably Table 5. In another embodiment, said composition comprises a nucleic acid comprising a sequence encoding an angiogenesis modulating protein, preferably selected from the group consisting of AAA4, AAA1, Edg-1, alpha 5 beta1 integrin, endomucin and matrix metalloproteinase 10, or fragment thereof, and a pharmaceutically acceptable carrier.

In another embodiment the nucleic acid selected from Tables 1, 2, 3, 4 or 5. Preferred nucleic acids are in Table 4, and most preferably Table 5.

A method of neutralizing the effect of an angiogenesis protein, preferably selected from the group consisting of AAA4, AAA1, Edg-1, alpha 5 beta1 integrin, endomucin and matrix metalloproteinase 10, or fragment thereof, comprising contacting an agent specific for said protein with said protein in an amount sufficient to effect neutralization. In another embodiment, the proteins is encoded by a nucleic acid selected from Tables 1, 2, 3, 4 or 5. Preferred nucleic acids are in Table 4, and most preferably Table 5.

In another aspect of the invention, a method of treating an individual for a disorder associated with angiogenesis is provided. In one embodiment, the method comprises administering to said individual an inhibitor of Edg-1. In another embodiment, the method comprises administering to a patient having a disorder with angiogenesis an antibody to Edg-1 conjugated to a therapeutic moiety. Such a therapeutic moiety can be a cytotoxic agent or a radioisotope.

Novel sequences are provided herein. Compounds and compositions are also provided. Other aspects of the invention will become apparent to the skilled artisan by the following description of the invention.

DETAILED DESCRIPTION OF THE TABLES AND FIGURES

Table 1 provides the Accession numbers for 1774 genes, including expression sequence tags, (incorporated in their entirety here and throughout the application where Accession numbers are provided), whose expression levels change as a function of time in tissue undergoing angiogenesis compared to tissue that is not.

Table 2 provides the Accession numbers for a preferred subset of 559 genes, including expression sequence tags (incorporated in their entirety here and throughout the application where Accession numbers are provided), whose expression levels change as a function of time in tissue undergoing angiogenesis compared to tissue that is not. The sequences are characterized as predicted to encode secreted proteins (SS), or transmembrane proteins (TM) proteins.

Table 3 provides the Accession numbers for 1916 genes including expression sequence tags (incorporated in their entirety here and throughout the application where Accession numbers are provided), whose expression levels change as a function of time in tissue undergoing angiogenesis compared to tissue that is not.

Table 4 provides a preferred subset of 558 Accession numbers identified in Figure 4 whose expression levels change as a function of time in tissue undergoing angiogenesis compared to tissue that is not.

Table 5 provides a preferred subset of 20 Accession numbers identified in Figure 4 whose expression levels change as a function of time in tissue undergoing angiogenesis compared to tissue that is not.

Figure 1 is a graph of expression levels of sequences identified in Figure 1. Expression profiles are clustered into 4 groups. C1 (blue), C2 (red), C3 (green) and C4 (mustard).

Figure 2 shows an embodiment of a nucleic acid (mRNA) which includes a sequence encoding an angiogenesis protein, AAA4. The start and stop codons are underlined.

Figure 3 shows the open reading frame of a nucleic acid sequence encoding AAA4. The start and stop codons are underlined.

Figure 4 shows an embodiment of the amino acid sequence of AAA4. The signal peptide is double underlined, and the transmembrane sequence is underlined. In one embodiment herein, AAA4 is soluble. Thus, the signal peptide can be omitted, and the transmembrane domain deleted, inactivated, or truncated.

Figure 5 shows peptides AAA4p1 and AAA4p2.

Figure 6 shows the expression of AAA4 in angiogenesis models over time and in other, non-angiogenic tissues.

Figure 7 shows an embodiment of a nucleic acid sequence encoding an angiogenesis protein, AAA1. A putative stop codon is underlined.

Figure 8 shows an embodiment of an amino acid sequence for AAA1. A transmembrane domain is underlined. In one embodiment, AAA1 is soluble. In preferred embodiments, the transmembrane domain is deleted or inactivated, or AAA1 is truncated to delete the transmembrane domain.

Figure 9 shows AAA1p1 and AAA1p2.

Figure 10 shows a graph showing the relative expression of AAA1 in various tissues at different time points. "Exp 3" is an angiogenesis model showing tube formation over time using endothelial cells.

Figure 11 shows an embodiment of a nucleic acid, mRNA, which comprises a sequence encoding an angiogenesis protein, Edg-1. The start and stop codons are underlined.

Figure 12 shows the open reading frame encoding Edg-1, wherein the start and stop codons are underlined.

Figure 13 shows an embodiment of an amino acid sequence for an angiogenesis protein, Edg-1, wherein the transmembrane domains are underlined. In a preferred embodiment herein, a soluble form of Edg-1 is provided. In one embodiment, the transmembrane domains are deleted, inactivated, and/or the protein is truncated so as to exclude the domains (with or without re-ligation of remaining soluble regions).

Figure 14 depicts four peptide sequences provided herein and their respective solubilities.

Figure 15 shows the expression of Edg-1 over a variety of tissues.

Figure 16 shows the time course of induction of Edg-1 in a model for angiogenesis (Expt 1, Expt 2, Expt 3) in which low passage human endothelial cells form into tube structures over a period of a few

days in culture. The reproducible induction of Edg-1 occurred in a time frame consistent with its role in the tube forming process.

Figure 17 shows an embodiment of a nucleic acid sequence which includes the coding sequence for a tissue remodeling protein, alpha 5 beta 1 integrin (sometimes referred to as VLA-5), wherein the start and stop codon are underlined.

Figure 18 shows an embodiment of an amino acid sequence of a tissue remodeling protein, alpha 5 beta 1 integrin, wherein a transmembrane domain is underlined.

Figure 19 shows a bar graph depicting the results of 5 expression profiles of alpha 5 beta 1 integrin throughout the time course of tube formation. In particular, tube models 1, 2 and 3 show models which form tube structures from single isolated human endothelial cells; the "EC/PMA" model shows endothelial cells stimulated with pokeweed mitogen antigen, and the body atlas profile shows expression in various normal cell types and tissues.

Figures 20A and 20B show the results of antagonism of tube formation wherein Figure 20A is an isotype control and Figure 20B shows specific antibody antagonism after 48 hours.

Figure 21 shows an embodiment of a nucleic acid sequence which includes the coding sequence for an angiogenesis protein, endomucin, wherein the start and stop codon are boxed.

Figure 22 shows an embodiment of an amino acid sequence of an angiogenesis protein, endomucin, wherein a signal sequence is bolded and a transmembrane domain is underlined.

Figure 23 shows an embodiment of a nucleic acid sequence which includes the coding sequence for an angiogenesis protein, matrix metalloproteinase 10 (also called stromolysin 2), wherein the start and stop codon are boxed.

Figure 24 shows expression of matrix metalloproteinase 10 over a variety of tissues.

Figure 25 shows expression of matrix metalloproteinase 10 over a variety of tissues.

DETAILED DESCRIPTION OF THE INVENTION

In accordance with the objects outlined above, the present invention provides novel methods for diagnosis of disorders associated with angiogenesis (sometimes referred to herein as angiogenesis disorders or AD), as well as methods for screening for compositions which modulate angiogenesis. By "disorder associated with angiogenesis" or "disease associated with angiogenesis" herein is meant a disease state which is marked by either an excess or a deficit of vessel development. Angiogenesis disorders include, but are not limited to, cancer and proliferative diabetic retinopathy. Also provided are method for treating AD.

In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is unique to the state of the cell. That is, normal tissue may be distinguished from AD tissue. By comparing expression profiles of tissue in known different angiogenesis states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. The identification of sequences that are differentially expressed in angiogenic versus non-angiogenic tissue allows the use of this information in a number of ways. For example, the evaluation of a particular treatment regime may be evaluated: does a chemotherapeutic drug act to down-regulate angiogenesis and thus tumor growth or recurrence in a particular patient. Similarly, diagnosis may be done or confirmed by comparing patient samples with the known expression profiles. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; for example, screening can be done for drugs that suppress the angiogenic expression profile. This may be done by making biochips comprising sets of the important angiogenesis genes, which can then be used in these screens. These methods can also be done on the protein basis; that is, protein expression levels of the angiogenic proteins can be evaluated for diagnostic purposes or to screen candidate agents. In addition, the angiogenic nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense nucleic acids, or the angiogenic proteins (including antibodies and other modulators thereof) administered as therapeutic drugs.

Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in angiogenesis, herein termed "angiogenesis sequences". As outlined below, angiogenesis sequences include those that are up-regulated (i.e. expressed at a higher level) in disorders associated with angiogenesis, as well as those that are down-regulated (i.e. expressed at a lower level). In a preferred embodiment, the angiogenesis sequences are from humans; however, as

will be appreciated by those in the art, angiogenesis sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other angiogenesis sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc). Angiogenesis sequences from other organisms may be obtained using the techniques outlined below.

Angiogenesis sequences can include both nucleic acid and amino acid sequences. In a preferred embodiment, the angiogenesis sequences are recombinant nucleic acids. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed in vitro, in general, by the manipulation of nucleic acid by polymerases and endonucleases, in a form not normally found in nature. Thus an isolated nucleic acid, in a linear form, or an expression vector formed in vitro by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, i.e. using the in vivo cellular machinery of the host cell rather than in vitro manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention.

Similarly, a "recombinant protein" is a protein made using recombinant techniques, i.e. through the expression of a recombinant nucleic acid as depicted above. A recombinant protein is distinguished from naturally occurring protein by at least one or more characteristics. For example, the protein may be isolated or purified away from some or all of the proteins and compounds with which it is normally associated in its wild type host, and thus may be substantially pure. For example, an isolated protein is unaccompanied by at least some of the material with which it is normally associated in its natural state, preferably constituting at least about 0.5%, more preferably at least about 5% by weight of the total protein in a given sample. A substantially pure protein comprises at least about 75% by weight of the total protein, with at least about 80% being preferred, and at least about 90% being particularly preferred. The definition includes the production of an angiogenesis protein from one organism in a different organism or host cell. Alternatively, the protein may be made at a significantly higher concentration than is normally seen, through the use of an inducible promoter or high expression promoter, such that the protein is made at increased concentration levels. Alternatively, the protein may be in a form not normally found in nature, as in the addition of an epitope tag or amino acid substitutions, insertions and deletions, as discussed below.

In a preferred embodiment, the angiogenesis sequences are nucleic acids. As will be appreciated by those in the art and is more fully outlined below, angiogenesis sequences are useful in a variety of

applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications; for example, biochips comprising nucleic acid probes to the angiogenesis sequences can be generated. In the broadest sense, then, by "nucleic acid" or "oligonucleotide" or grammatical equivalents herein means at least two nucleotides covalently linked together. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, as outlined below, nucleic acid analogs are included that may have alternate backbones, comprising, for example, phosphoramidate (Beaucage et al., Tetrahedron 49(10):1925 (1993) and references therein; Letsinger, J. Org. Chem. 35:3800 (1970); Sprinzl et al., Eur. J. Biochem. 81:579 (1977); Letsinger et al., Nucl. Acids Res. 14:3487 (1986); Sawai et al, Chem. Lett. 805 (1984), Letsinger et al., J. Am. Chem. Soc. 110:4470 (1988); and Pauwels et al., Chemica Scripta 26:141 91986)), phosphorothioate (Mag et al., Nucleic Acids Res. 19:1437 (1991); and U.S. Patent No. 5,644,048), phosphorodithioate (Briu et al., J. Am. Chem. Soc. 111:2321 (1989), O-methylphophoroamidite linkages (see Eckstein, Oligonucleotides and Analogues: A Practical Approach, Oxford University Press), and peptide nucleic acid backbones and linkages (see Egholm, J. Am. Chem. Soc. 114:1895 (1992); Meier et al., Chem. Int. Ed. Engl. 31:1008 (1992); Nielsen, Nature, 365:566 (1993); Carlsson et al., Nature 380:207 (1996), all of which are incorporated by reference). Other analog nucleic acids include those with positive backbones (Denpcy et al., Proc. Natl. Acad. Sci. USA 92:6097 (1995); non-ionic backbones (U.S. Patent Nos. 5,386,023, 5,637,684, 5,602,240, 5,216,141 and 4,469,863; Kiedrowshi et al., Angew. Chem. Intl. Ed. English 30:423 (1991); Letsinger et al., J. Am. Chem. Soc. 110:4470 (1988); Letsinger et al., Nucleoside & Nucleotide 13:1597 (1994); Chapters 2 and 3, ASC Symposium Series 580, "Carbohydrate Modifications in Antisense Research", Ed. Y.S. Sanghui and P. Dan Cook; Mesmaeker et al., Bioorganic & Medicinal Chem. Lett. 4:395 (1994); Jeffs et al., J. Biomolecular NMR 34:17 (1994); Tetrahedron Lett. 37:743 (1996)) and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, ASC Symposium Series 580, "Carbohydrate Modifications in Antisense Research", Ed. Y.S. Sanghui and P. Dan Cook. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids (see Jenkins et al., Chem. Soc. Rev. (1995) pp169-176). Several nucleic acid analogs are described in Rawls, C & E News June 2, 1997 page 35. All of these references are hereby expressly incorporated by reference. These modifications of the ribose-phosphate backbone may be done for a variety of reasons, for example to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip.

As will be appreciated by those in the art, all of these nucleic acid analogs may find use in the present invention. In addition, mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in two advantages. First, the PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (Tm) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4°C drop in Tm for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9°C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. As will be appreciated by those in the art, the depiction of a single strand ("Watson") also defines the sequence of the other strand ("Crick"); thus the sequences described herein also includes the complement of the sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA or a hybrid, where the nucleic acid contains any combination of deoxyribo- and ribo-nucleotides, and any combination of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus for example the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

An angiogenesis sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the angiogenesis sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions.

The angiogenesis screen included comparing genes identified in an *in vitro* model of angiogenesis as described in Hiraoka, Cell 95:365 (1998), which is expressly incorporated by reference, with genes identified in controls. Samples of normal tissue and tissue undergoing angiogenesis are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated as is known in the art for the preparation of mRNA. Suitable biochips are commercially available, for example from Affymetrix. Gene expression profiles as described herein are generated and the data analyzed.

In a preferred embodiment, the genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, including, but not limited to lung, heart, brain, liver, breast, kidney, muscle, prostate, small intestine, large intestine, spleen, bone and placenta. In a preferred embodiment, those genes identified during the angiogenesis screen that are expressed in any significant amount in other tissues are removed from the profile, although in some embodiments, this is not necessary. That is, when screening for drugs, it is preferable that the target be disease specific, to minimize possible side effects.

In a preferred embodiment, angiogenesis sequences are those that are up-regulated in angiogenesis disorders; that is, the expression of these genes is higher in the disease tissue as compared to normal tissue. "Up-regulation" as used herein means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred. All accession numbers herein are for the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is known in the art, see, e.g., Benson, DA, et al., Nucleic Acids Research 26:1-7 (1998) and http://www.ncbi.nlm.nih.gov/. In addition, these genes were found to be expressed in a limited amount or not at all in heart, brain, lung, liver, breast, kidney, prostate, small intestine and spleen.

In a preferred embodiment, angiogenesis sequences are those that are down-regulated in the angiogenesis disorder; that is, the expression of these genes is lower in angiogenic tissue as compared to normal tissue. "Down-regulation" as used herein means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred.

Angiogenesis sequences according to the invention may be classified into discrete clusters of sequences based on common expression profiles of the sequences. Expression levels of angiogenesis sequences may increase or decrease as a function of time in a manner that correlates with the induction of angiogenesis. Alternatively, expression levels of angiogenesis sequences may both increase and decrease as a function of time. For example, expression levels of some angiogenesis sequences are temporarily induced or diminished during the switch to the angiogenesis phenotype, followed by a return to baseline expression levels. Table 1 depicts 1774 genes, the expression of which varies as a function of time in angiogenesis tissue when compared to normal tissue. Figure 1 depicts 4 discrete expression profiles of angiogenesis genes identified in Table 1.

A particularly preferred embodiment includes the sequences as described in Table 2 which depicts a preferred subset of 559 angiogenesis sequences, the expression of which is altered in angiogenesis when compared to normal tissue.

An additional embodiment includes the sequences as described in Table 3, which depicts 1916 genes including expression sequence tags (incorporated in their entirety here and throughout the application where Accession numbers are provided), whose expression levels change as a function of time in tissue undergoing angiogenesis compared to tissue that is not.

A preferred embodiment includes the sequences as described in Table 4 which depicts a preferred subset of 558 genes identified in Table 3 whose expression levels change as a function of time in tissue undergoing angiogenesis compared to tissue that is not.

A particularly preferred embodiment includes the sequences as described in Table 5 which provides a preferred subset of 20 Accession numbers identified in Table 3 whose expression levels change as a function of time in tissue undergoing angiogenesis compared to tissue that is not.

In a particularly preferred embodiment, angiogenesis sequences are those that are induced for a period of time followed by a return to the baseline levels. Sequences that are temporarily induced provide a means to target angiogenesis tissue, for example neovascularized tumors, while avoiding rapidly growing tissue that require perpetual vascularization. Such positive angiogenic factors include aFGF, bFGF, VEGF, angiogenin and the like.

Induced angiogenesis sequences also are further categorized with respect to the timing of induction. For example, some angiogenesis genes may be induced at an early time period, such as with 10 minutes of the induction of angiogenesis. Others may be induced later, such as between 5 and 60 minutes, while yet others may be induced for a time period of about two hours or more followed by a return to baseline expression levels.

In another preferred embodiment are angiogenesis sequences that are inhibited or reduced as a function of time followed by a return to "normal" expression levels. Inhibitors of angiogenesis are examples of molecules that have this expression profile. These sequences also can be further divided into groups depending on the timing of diminished expression. For example, some molecules may display reduced expression with 10 minutes of the induction of angiogenesis. Others may be diminished later, such as between 5 and 60 minutes, while others may be diminished for a time period of about two hours or more followed by a return to baseline. Examples of such negative angiogenic factors include thrombospondin and endostatin to name a few.

In yet another preferred embodiment are angiogenesis sequences that are induced for prolonged periods. These sequences are typically associated with induction of angiogenesis and may participate in induction and/or maintenance of the angiogenesis phenotype.

In another preferred embodiment are angiogenesis sequences, the expression of which is reduced or diminished for prolonged periods in angiogenic tissue. These sequences are typically angiogenesis inhibitors and their diminution is correlated with an increase in angiogenesis.

Angiogenesis proteins of the present invention may be classified as secreted proteins, transmembrane proteins or intracellular proteins. In a preferred embodiment the angiogenesis protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleos. Intracellular proteins are involved in all aspects of cellular function and replication (including, for example, signaling pathways); aberrant expression of such proteins results in unregulated or disregulated cellular processes. For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing intracellular proteins is the presence in the proteins of one or more motifs for which defined functions have been attributed. In addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2 domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. As will be appreciated by one of ordinary skill in the art, these motifs can be identified on the basis of primary sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate.

In a preferred embodiment, the angiogenesis sequences are transmembrane proteins. Transmembrane proteins are molecules that span the phospholipid bilayer of a cell. They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For

example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Important transmembrane protein receptors include, but are not limited to insulin receptor, insulin-like growth factor receptor, human growth hormone receptor, glucose transporters, transferrin receptor, epidermal growth factor receptor, low density lipoprotein receptor, epidermal growth factor receptor, leptin receptor, interleukin receptors, e.g. IL-1 receptor, IL-2 receptor, etc.

Characteristics of transmembrane domains include approximately 20 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the localization and number of transmembrane domains within the protein may be predicted.

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. For example, cytokine receptors are characterized by a cluster of cysteines and a WSXWS (W= tryptophan, S= serine, X=any amino acid) motif. Immunoglobulin-like domains are highly conserved. Mucin-like domains may be involved in cell adhesion and leucine-rich repeats participate in protein-protein interactions.

Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, neurotrophic factors and the like. Extracellular domains also bind to cell-associated molecules. In this respect, they mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell for

example via a glycosylphosphatidylinositol (GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

Putative transmembrane angiogenesis proteins include those encoded by the sequences labeled with "Y" in the TM column depicted in Table 2.

Angiogenesis proteins that are transmembrane are particularly preferred in the present invention as they are good targets for immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities.

It will also be appreciated by those in the art that a transmembrane protein can be made soluble by removing transmembrane sequences, for example through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

In a preferred embodiment, the angiogenesis proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; by virtue of their circulating nature, they serve to transmit signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor) or an endocrine manner (acting on cells at a distance). Thus secreted molecules find use in modulating or altering numerous aspects of physiology. Angiogenesis proteins that are secreted proteins are particularly preferred in the present invention as they serve as good targets for diagnostic markers, for example for blood tests.

Putative secreted angiogenesis proteins include those encoded by the sequences depicted in Table 2 that are labeled with "Y" in the SS column, but a "N" in the TM column.

An angiogenesis sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology to the angiogenesis sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions.

As used herein, a nucleic acid is an "angiogenesis nucleic acid" if the overall homology of the nucleic acid sequence to one of the nucleic acids of Table 1, Table 2, Table 3, Table 4 or Table 5 is preferably greater than about 75%, more preferably greater than about 80%, even more preferably greater than about 85% and most preferably greater than 90%. In some embodiments the homology will be as high as about 93 to 95 or 98%. Homology in this context means sequence similarity or identity, with identity being preferred. A preferred comparison for homology purposes is to compare the sequence containing sequencing errors to the correct sequence. This homology will be determined using standard techniques known in the art, including, but not limited to, the local homology algorithm of Smith & Waterman, Adv. Appl. Math. 2:482 (1981), by the homology alignment algorith of Needleman & Wunsch, J. Mol. Biool. 48:443 (1970), by the search for similarity method of Pearson & Lipman, PNAS USA 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Drive, Madison, WI), the Best Fit sequence program described by Devereux et al., Nucl. Acid Res. 12:387-395 (1984), preferably using the default settings, or by inspection.

In a preferred embodiment, the sequences which are used to determine sequence identity or similarity are selected from the sequences set forth in the tables and figures, preferable those represented in Table 4, more preferably those represented in table 5, still more preferably those of Figures 2, 3, 7, 11, 12, 17, 21, 23 and fragments thereof. In one embodiment the sequences utilized herein are those set forth in the tables and figures. In another embodiment, the sequences are naturally occurring allelic variants of the sequences set forth in the tables and figures. In another embodiment, the sequences are sequence variants as further described herein.

One example of a useful algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pairwise alignments. It can also plot a tree showing the clustering relationships used to create the alignment. PILEUP uses a simplification of the progressive alignment method of Feng & Doolittle, J. Mol. Evol. 35:351-360 (1987); the method is similar to that described by Higgins & Sharp CABIOS 5:151-153 (1989). Useful PILEUP parameters including a default gap weight of 3.00, a default gap length weight of 0.10, and weighted end gaps.

Another example of a useful algorithm is the BLAST algorithm, described in Altschul et al., J. Mol. Biol. 215, 403-410, (1990) and Karlin et al., PNAS USA 90:5873-5787 (1993). A particularly useful BLAST program is the WU-BLAST-2 program which was obtained from Altschul et al., Methods in Enzymology, 266: 460-480 (1996); http://blast.wustl]. WU-BLAST-2 uses several search parameters, most of which are set to the default values. The adjustable parameters are set with the following values: overlap span =1, overlap fraction = 0.125, word threshold (T) = 11. The HSP S and HSP S2

parameters are dynamic values and are established by the program itself depending upon the composition of the particular sequence and composition of the particular database against which the sequence of interest is being searched; however, the values may be adjusted to increase sensitivity. A % amino acid sequence identity value is determined by the number of matching identical residues divided by the total number of residues of the "longer" sequence in the aligned region. The "longer" sequence is the one having the most actual residues in the aligned region (gaps introduced by WU-Blast-2 to maximize the alignment score are ignored).

Thus, "percent (%) nucleic acid sequence identity" is defined as the percentage of nucleotide residues in a candidate sequence that are identical with the nucleotide residues of the nucleic acids of the figures. A preferred method utilizes the BLASTN module of WU-BLAST-2 set to the default parameters, with overlap span and overlap fraction set to 1 and 0.125, respectively.

The alignment may include the introduction of gaps in the sequences to be aligned. In addition, for sequences which contain either more or fewer nucleotides than those of the nucleic acids of the figures, it is understood that the percentage of homology will be determined based on the number of homologous nucleosides in relation to the total number of nucleosides. Thus, for example, homology of sequences shorter than those of the sequences identified herein and as discussed below, will be determined using the number of nucleosides in the shorter sequence.

In one embodiment, the nucleic acid homology is determined through hybridization studies. Thus, for example, nucleic acids which hybridize under high stringency to the nucleic acids identified in the figures, or their complements, are considered an angiogenesis sequence. High stringency conditions are known in the art; see for example Maniatis et al., Molecular Cloning: A Laboratory Manual, 2d Edition, 1989, and Short Protocols in Molecular Biology, ed. Ausubel, et al., both of which are hereby incorporated by reference. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in Tijssen, Techniques in Biochemistry and Molecular Biology--Hybridization with Nucleic Acid Probes, "Overview of principles of hybridization and the strategy of nucleic acid assays" (1993). Generally, stringent conditions are selected to be about 5-10°C lower than the thermal melting point (Tm) for the specific sequence at a defined ionic strength pH. The Tm is the temperature (under defined ionic strength, pH and nucleic acid concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at Tm, 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH

7.0 to 8.3 and the temperature is at least about 30°C for short probes (e.g. 10 to 50 nucleotides) and at least about 60°C for long probes (e.g. greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide.

In another embodiment, less stringent hybridization conditions are used; for example, moderate or low stringency conditions may be used, as are known in the art; see Maniatis and Ausubel, supra, and Tijssen, supra.

In addition, the angiogenesis nucleic acid sequences of the invention are fragments of larger genes, i.e. they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, as will be appreciated by those in the art, using the sequences provided herein, additional sequences of the angiogenesis genes can be obtained, using techniques well known in the art for cloning either longer sequences or the full length sequences; see Maniatis et al., and Ausubel, et al., supra, hereby expressly incorporated by reference.

Once the angiogenesis nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire angiogenesis nucleic acid. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant angiogenesis nucleic acid can be further-used as a probe to identify and isolate other angiogenesis nucleic acids, for example additional coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant angiogenesis nucleic acids and proteins.

The angiogenesis nucleic acids of the present invention are used in several ways. In a first embodiment, nucleic acid probes to the angiogenesis nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, for example for gene therapy and/or antisense applications. Alternatively, the angiogenesis nucleic acids that include coding regions of angiogenesis proteins can be put into expression vectors for the expression of angiogenesis proteins, again either for screening purposes or for administration to a patient.

In a preferred embodiment, nucleic acid probes to angiogenesis nucleic acids (both the nucleic acid sequences outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the angiogenesis nucleic acids, i.e. the target sequence (either the target sequence of the sample or to other probe sequences, for example in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect;

there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under normal reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8 to about 100 bases long, with from about 10 to about 80 bases being preferred, and from about 30 to about 50 bases being particularly preferred. That is, generally whole genes are not used. In some embodiments, much longer nucleic acids can be used, up to hundreds of bases.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a particular target. The probes can be overlapping (i.e. have some sequence in common), or separate.

As will be appreciated by those in the art, nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined below. The binding can be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is meant one or more of either electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent attachment of a molecule, such as, streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to the biochip in a wide variety of ways, as will be appreciated by those in the art. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant any material that can be modified to contain discrete individual sites appropriate for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. As will be appreciated by those in the art, the number of possible substrates are very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, TeflonJ, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluorescese. A preferred substrate is described in copending application entitled Reusable Low Fluorescent Plastic Biochip, U.S. Application Serial No. 09/270,214, filed March 15, 1999, herein incorporated by reference in its entirety.

Generally the substrate is planar, although as will be appreciated by those in the art, other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube, for flow-through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, for example, the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, for example using linkers as are known in the art; for example, homo-or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200, incorporated herein by reference). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, the oligonucleotides are synthesized as is known in the art, and then attached to the surface of the solid support. As will be appreciated by those skilled in the art, either the 5' or 3' terminus may be attached to the solid support, or attachment may be via an internal nucleoside.

In an additional embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface, as is known in the art. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized in situ, using well known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affimetrix GeneChip™ technology.

In a preferred embodiment, angiogenesis nucleic acids encoding angiogenesis proteins are used to make a variety of expression vectors to express angiogenesis proteins which can then be used in screening assays, as described below. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the angiogenesis protein. The term "control sequences" refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. The transcriptional and translational regulatory nucleic acid

will generally be appropriate to the host cell used to express the angiogenesis protein; for example, transcriptional and translational regulatory nucleic acid sequences from *Bacillus* are preferably used to express the angiogenesis protein in *Bacillus*. Numerous types of appropriate expression vectors, and suitable regulatory sequences are known in the art for a variety of host cells.

In general, the transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences encode either constitutive or inducible promoters. The promoters may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known in the art, and are useful in the present invention.

In addition, the expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, for example in mammalian or insect cells for expression and in a procaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are well known in the art.

In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known in the art and will vary with the host cell used.

The angiogenesis proteins of the present invention are produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding an angiogenesis protein, under the appropriate conditions to induce or cause expression of the angiogenesis protein. The conditions appropriate for angiogenesis protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained by one skilled in the art through routine experimentation. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the

harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaebacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are *Drosophila melangaster* cells, *Saccharomyces cerevisiae* and other yeasts, *E. coli*, *Bacillus subtilis*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells),THP1 cells (a macrophage cell line) and human cells and lines.

In a preferred embodiment, the angiogenesis proteins are expressed in mammalian cells. Mammalian expression systems are also known in the art, and include retroviral systems. A preferred expression vector system is a retroviral vector system such as is generally described in PCT/US97/01019 and PCT/US97/01048, both of which are hereby expressly incorporated by reference. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter. Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenlytion signals include those derived form SV40.

The methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, is well known in the art, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

In a preferred embodiment, angiogenesis proteins are expressed in bacterial systems. Bacterial expression systems are well known in the art. Promoters from bacteriophage may also be used and are known in the art. In addition, synthetic promoters and hybrid promoters are also useful; for example, the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the angiogenesis protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located

between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known in the art, and include vectors for *Bacillus subtilis*, *E. coli*, *Streptococcus cremoris*, and *Streptococcus lividans*, among others. The bacterial expression vectors are transformed into bacterial host cells using techniques well known in the art, such as calcium chloride treatment, electroporation, and others.

In one embodiment, angiogenesis proteins are produced in insect cells. Expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors, are well known in the art.

In a preferred embodiment, angiogenesis protein is produced in yeast cells. Yeast expression systems are well known in the art, and include expression vectors for *Saccharomyces cerevisiae*, *Candida albicans* and *C. maltosa*, *Hansenula polymorpha*, *Kluyveromyces fragilis* and *K. lactis*, *Pichia guillerimondii* and *P. pastoris*, *Schizosaccharomyces pombe*, and *Yarrowia lipolytica*.

The angiogenesis protein may also be made as a fusion protein, using techniques well known in the art. Thus, for example, for the creation of monoclonal antibodies, if the desired epitope is small, the angiogenesis protein may be fused to a carrier protein to form an immunogen. Alternatively, the angiogenesis protein may be made as a fusion protein to increase expression, or for other reasons. For example, when the angiogenesis protein is an angiogenesis peptide, the nucleic acid encoding the peptide may be linked to other nucleic acid for expression purposes.

In one embodiment, the angiogenesis nucleic acids, proteins and antibodies of the invention are labeled. By "labeled" herein is meant that a compound has at least one element, isotope or chemical compound attached to enable the detection of the compound. In general, labels fall into three classes: a) isotopic labels, which may be radioactive or heavy isotopes; b) immune labels, which may be antibodies or antigens; and c) colored or fluorescent dyes. The labels may be incorporated into the angiogenesis nucleic acids, proteins and antibodies at any position. For example, the label should be capable of producing, either directly or indirectly, a detectable signal. The detectable moiety may be a radioisotope, such as ^{3}H, ^{14}C, ^{32}P, ^{35}S, or ^{125}I, a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme, such as alkaline phosphatase, beta-

galactosidase or horseradish peroxidase. Any method known in the art for conjugating the antibody to the label may be employed, including those methods described by Hunter et al., Nature, 144:945 (1962); David et al., Biochemistry, 13:1014 (1974); Pain et al., J. Immunol. Meth., 40:219 (1981); and Nygren, J. Histochem. and Cytochem., 30:407 (1982).

Accordingly, the present invention also provides angiogenesis protein sequences. An angiogenesis protein of the present invention may be identified in several ways. "Protein" in this sense includes proteins, polypeptides, and peptides. As will be appreciated by those in the art, the nucleic acid sequences of the invention can be used to generate protein sequences. There are a variety of ways to do this, including cloning the entire gene and verifying its frame and amino acid sequence, or by comparing it to known sequences to search for homology to provide a frame, assuming the angiogenesis protein has homology to some protein in the database being used. Generally, the nucleic acid sequences are input into a program that will search all three frames for homology. This is done in a preferred embodiment using the following NCBI Advanced BLAST parameters. The program is blastx or blastn. The database is nr. The input data is as "Sequence in FASTA format". The organism list is "none". The "expect" is 10; the filter is default. The "descriptions" is 500, the "alignments" is 500, and the "alignment view" is pairwise. The "Query Genetic Codes" is standard (1). The matrix is BLOSUM62; gap existence cost is 11, per residue gap cost is 1; and the lambda ratio is .85 default. This results in the generation of a putative protein sequence.

Also included within one embodiment of angiogenesis proteins are amino acid variants of the naturally occurring sequences, as determined herein. Preferably, the variants are preferably greater than about 75% homologous to the wild-type sequence, more preferably greater than about 80%, even more preferably greater than about 85% and most preferably greater than 90%. In some embodiments the homology will be as high as about 93 to 95 or 98%. As for nucleic acids, homology in this context means sequence similarity or identity, with identity being preferred. This homology will be determined using standard techniques known in the art as are outlined above for the nucleic acid homologies.

Angiogenesis proteins of the present invention may be shorter or longer than the wild type amino acid sequences. Thus, in a preferred embodiment, included within the definition of angiogenesis proteins are portions or fragments of the wild type sequences. herein. In addition, as outlined above, the angiogenesis nucleic acids of the invention may be used to obtain additional coding regions, and thus additional protein sequence, using techniques known in the art.

In a preferred embodiment, the angiogenesis proteins are derivative or variant angiogenesis proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative

angiogenesis peptide will contain at least one amino acid substitution, deletion or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion or deletion may occur at any residue within the angiogenesis peptide.

Also included within one embodiment of angiogenesis proteins of the present invention are amino acid sequence variants. These variants fall into one or more of three classes: substitutional, insertional or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the angiogenesis protein, using cassette or PCR mutagenesis or other techniques well known in the art, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant angiogenesis protein fragments having up to about 100-150 residues may be prepared by in vitro synthesis using established techniques. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the angiogenesis protein amino acid sequence. The variants typically exhibit the same qualitative biological activity as the naturally occurring analogue, although variants can also be selected which have modified characteristics as will be more fully outlined below.

While the site or region for introducing an amino acid sequence variation is predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed angiogenesis variants screened for the optimal combination of desired activity. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well known, for example, M13 primer mutagenesis and PCR mutagenesis. Screening of the mutants is done using assays of angiogenesis protein activities.

Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1 to 20 amino acids, although considerably larger insertions may be tolerated. Deletions range from about 1 to about 20 residues, although in some cases deletions may be much larger.

Substitutions, deletions, insertions or any combination thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the alteration of the molecule. However, larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of the angiogenesis protein are desired, substitutions are generally made in accordance with the following chart:

Chart I

Original Residue	Exemplary Substitutions
Ala	Ser
Arg	Lys
Asn	Gln, His
Asp	Glu
Cys	Ser
Gln	Asn
Glu	Asp
Gly	Pro
His	Asn, Gln
Ile	Leu, Val
Leu	Ile, Val
Lys	Arg, Gln, Glu
Met	Leu, Ile
Phe	Met, Leu, Tyr
Ser	Thr
Thr	Ser
Trp	Tyr
Tyr	Trp, Phe
Val	Ile, Leu

Substantial changes in function or immunological identity are made by selecting substitutions that are less conservative than those shown in Chart I. For example, substitutions may be made which more significantly affect: the structure of the polypeptide backbone in the area of the alteration, for example the alpha-helical or beta-sheet structure; the charge or hydrophobicity of the molecule at the target site; or the bulk of the side chain. The substitutions which in general are expected to produce the greatest changes in the polypeptide's properties are those in which (a) a hydrophilic residue, e.g. seryl or threonyl, is substituted for (or by) a hydrophobic residue, e.g. leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side chain, e.g. lysyl, arginyl, or histidyl, is substituted for (or by) an electronegative residue, e.g. glutamyl or aspartyl; or (d) a residue having a bulky side chain, e.g. phenylalanine, is substituted for (or by) one not having a side chain, e.g. glycine.

The variants typically exhibit the same qualitative biological activity and will elicit the same immune response as the naturally-occurring analogue, although variants also are selected to modify the characteristics of the angiogenesis proteins as needed. Alternatively, the variant may be designed such that the biological activity of the angiogenesis protein is altered. For example, glycosylation sites may be altered or removed.

Covalent modifications of angiogenesis polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of an angiogenesis

polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of an angiogenesis polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking angiogenesis polypeptides to a water-insoluble support matrix or surface for use in the method for purifying anti-angiogenesis polypeptide antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-[(p-azidophenyl)dithio]propioimidate.

Other modifications include deamidation of glutaminyl and asparaginyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl, threonyl or tyrosyl residues, methylation of the α-amino groups of lysine, arginine, and histidine side chains [T.E. Creighton, Proteins: Structure and Molecular Properties, W.H. Freeman & Co., San Francisco, pp. 79-86 (1983)], acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the angiogenesis polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence angiogenesis polypeptide, and/or adding one or more glycosylation sites that are not present in the native sequence angiogenesis polypeptide.

Addition of glycosylation sites to angiogenesis polypeptides may be accomplished by altering the amino acid sequence thereof. The alteration may be made, for example, by the addition of, or substitution by, one or more serine or threonine residues to the native sequence angiogenesis polypeptide (for O-linked glycosylation sites). The angiogenesis amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the angiogenesis polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the angiogenesis polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330 published 11 September 1987, and in Aplin and Wriston, CRC Crit. Rev. Biochem., pp. 259-306 (1981).

Removal of carbohydrate moieties present on the angiogenesis polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al., Arch. Biochem. Biophys., 259:52 (1987) and by Edge et al., Anal. Biochem., 118:131 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and exo-glycosidases as described by Thotakura et al., Meth. Enzymol., 138:350 (1987).

Another type of covalent modification of angiogenesis comprises linking the angiogenesis polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337.

Angiogenesis polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising an angiogenesis polypeptide fused to another, heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of an angiogenesis polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino-or carboxyl-terminus of the angiogenesis polypeptide. The presence of such epitope-tagged forms of an angiogenesis polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the angiogenesis polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of an angiogenesis polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; the flu HA tag polypeptide and its antibody 12CA5 [Field et al., Mol. Cell. Biol., 8:2159-2165 (1988)]; the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto [Evan et al., Molecular and Cellular Biology, 5:3610-3616 (1985)]; and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody [Paborsky et al., Protein Engineering, 3(6):547-553 (1990)]. Other tag polypeptides include the Flag-peptide [Hopp et al., BioTechnology, 6:1204-1210 (1988)]; the KT3 epitope peptide [Martin et al., Science, 255:192-194 (1992)]; tubulin epitope peptide [Skinner et al., J. Biol. Chem., 266:15163-15166 (1991)]; and the T7 gene 10 protein peptide tag [Lutz-Freyermuth et al., Proc. Natl. Acad. Sci. USA, 87:6393-6**397 (1990)].

Also included with an embodiment of angiogenesis protein are other angiogenesis proteins of the angiogenesis family, and angiogenesis proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related angiogenesis proteins from humans or other organisms. As will be appreciated by those in the art, particularly useful probe and/or PCR primer sequences include the unique areas of the angiogenesis nucleic acid sequence. As is generally known in the art, preferred PCR primers are from about 15 to about 35 nucleotides in length, with from about 20 to about 30 being preferred, and may contain inosine as needed. The conditions for the PCR reaction are well known in the art.

In addition, as is outlined herein, angiogenesis proteins can be made that are longer than those encoded by the nucleic acids of the figures, for example, by the elucidation of additional sequences, the addition of epitope or purification tags, the addition of other fusion sequences, etc.

Angiogenesis proteins may also be identified as being encoded by angiogenesis nucleic acids. Thus, angiogenesis proteins are encoded by nucleic acids that will hybridize to the sequences of the sequence listings, or their complements, as outlined herein.

In a preferred embodiment, when the angiogenesis protein is to be used to generate antibodies, for example for immunotherapy, the angiogenesis protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller angiogenesis protein will be able to bind to the full length protein. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity. In a preferred embodiment, the epitope is selected from AAA4p1 and AAA4p2. In another preferred embodiment the epitope is selected from AAA1p1 and AAA1p2. In another preferred embodiment the epitope is selected from AAA7p1, AAA7p2, AAA7p3 and AAA7p1m.

In one embodiment, the term "antibody" includes antibody fragments, as are known in the art, including Fab, Fab_2, single chain antibodies (Fv for example), chimeric antibodies, etc., either produced by the modification of whole antibodies or those synthesized de novo using recombinant DNA technologies.

Methods of preparing polyclonal antibodies are known to the skilled artisan. Polyclonal antibodies can be raised in a mammal, for example, by one or more injections of an immunizing agent and, if desired,

an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a nucleic acid of the figures or fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art without undue experimentation.

The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized *in vitro*. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of Table 1, Table 2, Table 3, Table 4 or Table 5 or fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell [Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103]. Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for a protein encoded by a nucleic acid of figure 1 or 3-6 or a fragment thereof, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific.

In a preferred embodiment, the antibodies to angiogenesis protein are capable of reducing or eliminating the biological function of angiogenesis protein, as is described below. That is, the addition of anti-angiogenesis protein antibodies (either polyclonal or preferably monoclonal) to angiogenic tissue (or cells containing angiogenesis) may reduce or eliminate the angiogenesis activity. Generally, at least a 25% decrease in activity is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

In a preferred embodiment the antibodies to the angiogenesis proteins are humanized antibodies. Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', $F(ab')_2$ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues form a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin [Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-329 (1988); and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)].

Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues are often referred to as import residues, which are typically taken from an import variable domain. Humanization can be essentially performed following the method of Winter and co-workers [Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeyen et al., Science, 239:1534-1536 (1988)], by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some

CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

Human antibodies can also be produced using various techniques known in the art, including phage display libraries [Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991)]. The techniques of Cole et al. and Boerner et al. are also available for the preparation of human monoclonal antibodies (Cole et al., Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, p. 77 (1985) and Boerner et al., J. Immunol., 147(1):86-95 (1991)]. Similarly, human antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks et al., Bio/Technology 10, 779-783 (1992); Lonberg et al., Nature 368 856-859 (1994); Morrison, Nature 368, 812-13 (1994); Fishwild et al., Nature Biotechnology 14, 845-51 (1996); Neuberger, Nature Biotechnology 14, 826 (1996); Lonberg and Huszar, Intern. Rev. Immunol. 13 65-93 (1995).

By immunotherapy is meant treatment of angiogenesis with an antibody raised against angiogenesis proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. As appreciated by one of ordinary skill in the art, the antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen.

In a preferred embodiment the angiogenesis proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment, bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted angiogenesis protein.

In another preferred embodiment, the angiogenesis protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment, bind the extracellular domain of the angiogenesis protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The antibody may cause down-regulation of the

transmembrane angiogenesis protein. As will be appreciated by one of ordinary skill in the art, the antibody may be a competitive, non-competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the angiogenesis protein. The antibody is also an antagonist of the angiogenesis protein. Further, the antibody prevents activation of the transmembrane angiogenesis protein. In one aspect, when the antibody prevents the binding of other molecules to the angiogenesis protein, the antibody prevents growth of the cell. The antibody also sensitizes the cell to cytotoxic agents, including, but not limited to TNF-α, TNF-β, IL-1, INF-γ and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody belongs to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity. Thus, angiogenesis is treated by administering to a patient antibodies directed against the transmembrane angiogenesis protein.

In another preferred embodiment, the antibody is conjugated to a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of the angiogenesis protein. In another aspect the therapeutic moiety modulates the activity of molecules associated with or in close proximity to the angiogenesis protein. The therapeutic moiety may inhibit enzymatic activity such as protease or collagenase activity associated with angiogenesis.

In a preferred embodiment, the therapeutic moiety may also be a cytotoxic agent. In this method, targeting the cytotoxic agent to angiogenesis tissue or cells, results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with angiogenesis. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diptheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against angiogenesis proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane angiogenesis proteins not only serves to increase the local concentration of therapeutic moiety in the angiogenesis afflicted area, but also serves to reduce deleterious side effects that may be associated with the therapeutic moiety.

In another preferred embodiment, the angiogenesis protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the

angiogenesis protein can be targeted within a cell, i.e., the nucleus, an antibody thereto contains a signal for that target localization, i.e., a nuclear localization signal.

The angiogenesis antibodies of the invention specifically bind to angiogenesis proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a binding constant in the range of at least 10^{-4}- 10^{-6} M^{-1}, with a preferred range being 10^{-7} - 10^{-9} M^{-1}.

In a preferred embodiment, the angiogenesis protein is purified or isolated after expression. Angiogenesis proteins may be isolated or purified in a variety of ways known to those skilled in the art depending on what other components are present in the sample. Standard purification methods include electrophoretic, molecular, immunological and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the angiogenesis protein may be purified using a standard anti-angiogenesis protein antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. For general guidance in suitable purification techniques, see Scopes, R., Protein Purification, Springer-Verlag, NY (1982). The degree of purification necessary will vary depending on the use of the angiogenesis protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the angiogenesis proteins and nucleic acids are useful in a number of applications.

In one aspect, the expression levels of genes are determined for different cellular states in the angiogenesis phenotype; that is, the expression levels of genes in normal tissue (i.e. not undergoing angiogenesis) and in angiogenesis tissue (and in some cases, for varying severities of angiogenesis that relate to prognosis, as outlined below) are evaluated to provide expression profiles. An expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is unique to the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be done or confirmed: does tissue from a particular patient have the gene expression profile of normal or angiogenesis tissue.

"Differential expression," or grammatical equivalents as used herein, refers to both qualitative as well as quantitative differences in the genes' temporal and/or cellular expression patterns within and among the cells. Thus, a differentially expressed gene can qualitatively have its expression altered,

including an activation or inactivation, in, for example, normal versus angiogenic tissue. That is, genes may be turned on or turned off in a particular state, relative to another state. As is apparent to the skilled artisan, any comparison of two or more states can be made. Such a qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques in one such state or cell type, but is not detectable in both. Alternatively, the determination is quantitative in that expression is increased or decreased; that is, the expression of the gene is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays, Lockhart, Nature Biotechnology, 14:1675-1680 (1996), hereby expressly incorporated by reference. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, Northern analysis and RNase protection. As outlined above, preferably the change in expression (i.e. upregulation or downregulation) is at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably, at least about 200%, with from 300 to at least 1000% being especially preferred.

As will be appreciated by those in the art, this may be done by evaluation at either the gene transcript, or the protein level; that is, the amount of gene expression may be monitored using nucleic acid probes to the DNA or RNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, for example through the use of antibodies to the angiogenesis protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Thus, the proteins corresponding to angiogenesis genes, i.e. those identified as being important in an angiogenesis phenotype, can be evaluated in an angiogenesis diagnostic test.

In a preferred embodiment, gene expression monitoring is done and a number of genes, i.e. an expression profile, is monitored simultaneously, although multiple protein expression monitoring can be done as well. Similarly, these assays may be done on an individual basis as well.

In this embodiment, the angiogenesis nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of angiogenesis sequences in a particular cell. The assays are further described below in the example.

In a preferred embodiment nucleic acids encoding the angiogenesis protein are detected. Although DNA or RNA encoding the angiogenesis protein may be detected, of particular interest are methods wherein the mRNA encoding an angiogenesis protein is detected. The presence of mRNA in a

sample is an indication that the angiogenesis gene has been transcribed to form the mRNA, and suggests that the protein is expressed. Probes to detect the mRNA can be any nucleotide/deoxynucleotide probe that is complementary to and base pairs with the mRNA and includes but is not limited to oligonucleotides, cDNA or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method detection of the mRNA is performed in situ. In this method permeabilized cells or tissue samples are contacted with a detectably labeled nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxygenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding an angiogenesis protein is detected by binding the digoxygenin with an anti-digoxygenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl phosphate.

In a preferred embodiment, any of the three classes of proteins as described herein (secreted, transmembrane or intracellular proteins) are used in diagnostic assays. The angiogenesis proteins, antibodies, nucleic acids, modified proteins and cells containing angiogenesis sequences are used in diagnostic assays. This can be done on an individual gene or corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, angiogenesis proteins, including intracellular, transmembrane or secreted proteins, find use as markers of angiogenesis. Detection of these proteins in putative angiogenesis tissue or patients allows for a determination or diagnosis of angiogenesis. Numerous methods known to those of ordinary skill in the art find use in detecting angiogenesis. In one embodiment, antibodies are used to detect angiogenesis proteins. A preferred method separates proteins from a sample or patient by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be any other type of gel including isoelectric focusing gels and the like). Following separation of proteins, the angiogenesis protein is detected by immunoblotting with antibodies raised against the angiogenesis protein. Methods of immunoblotting are well known to those of ordinary skill in the art.

In another preferred method, antibodies to the angiogenesis protein find use in in situ imaging techniques. In this method cells are contacted with from one to many antibodies to the angiogenesis

protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a detectable label. In another method the primary antibody to the angiogenesis protein(s) contains a detectable label. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of angiogenesis proteins. As will be appreciated by one of ordinary skill in the art, numerous other histological imaging techniques are useful in the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

In another preferred embodiment, antibodies find use in diagnosing angiogenesis from blood samples. As previously described, certain angiogenesis proteins are secreted/circulating molecules. Blood samples, therefore, are useful as samples to be probed or tested for the presence of secreted angiogenesis proteins. Antibodies can be used to detect the angiogenesis by any of the previously described immunoassay techniques including ELISA, immunoblotting (Western blotting), immunoprecipitation, BIACORE technology and the like, as will be appreciated by one of ordinary skill in the art.

In a preferred embodiment, in situ hybridization of labeled angiogenesis nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including angiogenesis tissue and/or normal tissue, are made. In situ hybridization as is known in the art can then be done.

It is understood that when comparing the fingerprints between an individual and a standard, the skilled artisan can make a diagnosis as well as a prognosis. It is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis.

In a preferred embodiment, the angiogenesis proteins, antibodies, nucleic acids, modified proteins and cells containing angiogenesis sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to angiogenesis severity, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. As above, the angiogenesis probes are attached to biochips for the detection and quantification of angiogenesis sequences in a tissue or patient. The assays proceed as outlined above for diagnosis.

In a preferred embodiment any of the three classes of proteins as described herein are used in drug screening assays. The angiogenesis proteins, antibodies, nucleic acids, modified proteins and cells containing angiogenesis sequences are used in drug screening assays or by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, Zlokarnik, et al., Science 279, 84-8 (1998), Heid, 1996 #69.

In a preferred embodiment, the angiogenesis proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified angiogenesis proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the angiogenesis phenotype. As above, this can be done on an individual gene level or by evaluating the effect of drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, supra.

Having identified the differentially expressed genes herein, a variety of assays may be executed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene as up regulated in angiogenesis, candidate bioactive agents may be screened to modulate this gene's response; preferably to down regulate the gene, although in some circumstances to up regulate the gene. "Modulation" thus includes both an increase and a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal versus tissue undergoing angiogenesis, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4 fold increase in angiogenic tissue compared to normal tissue, a decrease of about four fold is desired; a 10 fold decrease in angiogenic tissue compared to normal tissue gives a 10 fold increase in expression for a candidate agent being desired.

As will be appreciated by those in the art, this may be done by evaluation at either the gene or the protein level; that is, the amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be monitored, for example through the use of antibodies to the angiogenesis protein and standard immunoassays.

In a preferred embodiment, gene expression monitoring is done and a number of genes, i.e. an expression profile, is monitored simultaneously, although multiple protein expression monitoring can be done as well.

In this embodiment, the angiogenesis nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of angiogenesis sequences in a particular cell. The assays are further described below.

Generally, in a preferred embodiment, a candidate bioactive agent is added to the cells prior to analysis. Moreover, screens are provided to identify a candidate bioactive agent which modulates angiogenesis, modulates angiogenesis proteins, binds to an angiogenesis protein, or interferes between the binding of an angiogenesis protein and an antibody.

The term "candidate bioactive agent" or "drug candidate" or grammatical equivalents as used herein describes any molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for bioactive agents that are capable of directly or indirectly altering either the angiogenesis phenotype or the expression of an angiogenesis sequence, including both nucleic acid sequences and protein sequences. In preferred embodiments, the bioactive agents modulate the expression profiles, or expression profile nucleic acids or proteins provided herein. In a particularly preferred embodiment, the candidate agent suppresses an angiogenesis phenotype, for example to a normal tissue fingerprint. Similarly, the candidate agent preferably suppresses a severe angiogenesis phenotype. Generally a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, i.e., at zero concentration or below the level of detection.

In one aspect, a candidate agent will neutralize the effect of an angiogenesis protein. By "neutralize" is meant that activity of a protein is either inhibited or counter acted against so as to have substantially no effect on a cell.

Candidate agents encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 100 and less than about 2,500 daltons. Preferred small molecules are less than 2000, or less than 1500 or less than 1000 or less than 500 D. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Candidate agents are also found among biomolecules including peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs or combinations thereof. Particularly preferred are peptides.

Candidate agents are obtained from a wide variety of sources including libraries of synthetic or natural compounds. For example, numerous means are available for random and directed synthesis of a wide variety of organic compounds and biomolecules, including expression of randomized oligonucleotides. Alternatively, libraries of natural compounds in the form of bacterial, fungal, plant and animal extracts are available or readily produced. Additionally, natural or synthetically produced libraries and compounds are readily modified through conventional chemical, physical and biochemical means. Known pharmacological agents may be subjected to directed or random chemical modifications, such as acylation, alkylation, esterification, amidification to produce structural analogs.

In a preferred embodiment, the candidate bioactive agents are proteins. By "protein" herein is meant at least two covalently attached amino acids, which includes proteins, polypeptides, oligopeptides and peptides. The protein may be made up of naturally occurring amino acids and peptide bonds, or synthetic peptidomimetic structures. Thus "amino acid", or "peptide residue", as used herein means both naturally occurring and synthetic amino acids. For example, homo-phenylalanine, citrulline and noreleucine are considered amino acids for the purposes of the invention. "Amino acid" also includes imino acid residues such as proline and hydroxyproline. The side chains may be in either the (R) or the (S) configuration. In the preferred embodiment, the amino acids are in the (S) or L-configuration. If non-naturally occurring side chains are used, non-amino acid substituents may be used, for example to prevent or retard in vivo degradations.

In a preferred embodiment, the candidate bioactive agents are naturally occurring proteins or fragments of naturally occurring proteins. Thus, for example, cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of procaryotic and eucaryotic proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred.

In a preferred embodiment, the candidate bioactive agents are peptides of from about 5 to about 30 amino acids, with from about 5 to about 20 amino acids being preferred, and from about 7 to about 15 being particularly preferred. The peptides may be digests of naturally occurring proteins as is outlined above, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that each nucleic acid and peptide consists of essentially random nucleotides and amino acids, respectively. Since generally these random peptides (or nucleic acids, discussed below) are chemically synthesized, they may incorporate any nucleotide or amino acid at any position. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the

formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. For example, in a preferred embodiment, the nucleotides or amino acid residues are randomized within a defined class, for example, of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines or histidines for phosphorylation sites, etc., or to purines, etc.

In a preferred embodiment, the candidate bioactive agents are nucleic acids, as defined above.

As described above generally for proteins, nucleic acid candidate bioactive agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. For example, digests of procaryotic or eucaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate bioactive agents are organic chemical moieties, a wide variety of which are available in the literature.

After the candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing the target sequences to be analyzed is added to the biochip. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR occurring as needed, as will be appreciated by those in the art. For example, an in vitro transcription with labels covalently attached to the nucleosides is done. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, for example, a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin.

For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. As known in the art, unbound labeled streptavidin is removed prior to analysis.

As will be appreciated by those in the art, these assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos. 5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246 and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

A variety of hybridization conditions may be used in the present invention, including high, moderate and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allows formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways, as will be appreciated by those in the art. Components of the reaction may be added simultaneously, or sequentially, in any order, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents may be included in the assays. These include reagents like salts, buffers, neutral proteins, e.g. albumin, detergents, etc which may be used to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used, depending on the sample preparation methods and purity of the target.

Once the assay is run, the data is analyzed to determine the expression levels, and changes in expression levels as between states, of individual genes, forming a gene expression profile.

The screens are done to identify drugs or bioactive agents that modulate the angiogenesis phenotype. Specifically, there are several types of screens that can be run. A preferred embodiment is in the screening of candidate agents that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. That is, candidate agents that can mimic or produce an expression profile in angiogenesis similar to the expression profile of normal tissue is expected to result in a suppression of the angiogenesis phenotype. Thus, in this embodiment, mimicking an expression profile, or changing one profile to another, is the goal.

In a preferred embodiment, as for the diagnosis applications, having identified the differentially expressed genes important in any one state, screens can be run to alter the expression of the genes individually. That is, screening for modulation of regulation of expression of a single gene can be done; that is, rather than try to mimic all or part of an expression profile, screening for regulation of individual genes can be done. Thus, for example, particularly in the case of target genes whose presence or absence is unique between two states, screening is done for modulators of the target gene expression.

In a preferred embodiment, screening is done to alter the biological function of the expression product of the differentially expressed gene. Again, having identified the importance of a gene in a particular state, screening for agents that bind and/or modulate the biological activity of the gene product can be run as is more fully outlined below.

Thus, screening of candidate agents that modulate the angiogenesis phenotype either at the gene expression level or the protein level can be done.

In addition screens can be done for novel genes that are induced in response to a candidate agent. After identifying a candidate agent based upon its ability to suppress an angiogenesis expression pattern leading to a normal expression pattern, or modulate a single angiogenesis gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated angiogenesis tissue reveals genes that are not expressed in normal tissue or angiogenesis tissue, but are expressed in agent treated tissue. These agent specific sequences can be identified and used by any of the methods described herein for angiogenesis genes or proteins. In particular these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics to the treated angiogenesis tissue sample.

Thus, in one embodiment, a candidate agent is administered to a population of angiogenic cells, that thus has an associated angiogenesis expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (i.e. a peptide) may be put into a viral construct such as a retroviral construct and added to the cell, such that expression of the peptide agent is accomplished; see PCT US97/01019, hereby expressly incorporated by reference.

Once the candidate agent has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

Thus, for example, angiogenesis tissue may be screened for agents that reduce or suppress the angiogenesis phenotype. A change in at least one gene of the expression profile indicates that the agent has an effect on angiogenesis activity. By defining such a signature for the angiogenesis phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of either the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "angiogenesis proteins". In preferred embodiments the angiogenesis protein is as depicted in Figures 4, 8, 13, 18, and 22 or encoded by the sequences shown in figures 2, 3, 7, 12, 17, 21 and 23. The angiogenesis protein may be a fragment, or alternatively, be the full length protein to a fragment shown herein.

Preferably, the angiogenesis protein is a fragment of approximately 14 to 24 amino acids long. More preferably the fragment is a soluble fragment.

In a preferred embodiment, the fragment is from AAA1. Preferably, the fragment includes a non-transmembrane region. In a preferred embodiment, the AAA1 fragment has an N-terminal Cys to aid in solubility. Preferably, the fragment is selected from AAA1p1 and AAA1p2.

In a preferred embodiment, the fragment is charged and from the c-terminus of AAA4. In one embodiment, the c-terminus of the fragment is kept as a free acid and the n-terminus is a free amine to aid in coupling, i.e., to cysteine. In one embodiment the fragment is an internal peptide overlapping hydrophilic stretch of AAA4. In a preferred embodiment, the termini is blocked. Preferably, the fragment of AAA4 is selected from AAA4p1 or AAA4p2. In another preferred embodiment, the fragment is a novel fragment from the N-terminal. In one embodiment, the fragment excludes sequence outside of the N-terminal, in another embodiment, the fragment includes at least a portion of the N-terminal. "N-terminal" is used interchangeably herein with "N-terminus" which is further described above.

In one embodiment the angiogenesis proteins are conjugated to an immunogenic agent as discussed herein. In one embodiment the angiogenesis protein is conjugated to BSA.

Thus, in a preferred embodiment, screening for modulators of expression of specific genes can be done. This will be done as outlined above, but in general the expression of only one or a few genes are evaluated.

In a preferred embodiment, screens are designed to first find candidate agents that can bind to differentially expressed proteins, and then these agents may be used in assays that evaluate the ability of the candidate agent to modulate differentially expressed activity. Thus, as will be appreciated by those in the art, there are a number of different assays which may be run; binding assays and activity assays.

In a preferred embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. In general, this is done as is known in the art. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the angiogenesis proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining an angiogenesis protein and a candidate bioactive agent, and determining the binding of the candidate agent to the angiogenesis protein. Preferred embodiments utilize the human angiogenesis protein, although other mammalian proteins may also be used, for example for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative angiogenesis proteins may be used.

Generally, in a preferred embodiment of the methods herein, the angiogenesis protein or the candidate agent is non-diffusably bound to an insoluble support having isolated sample receiving areas (e.g. a microtiter plate, an array, etc.). The insoluble supports may be made of any composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports may be solid or porous and of any convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflon™, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition is not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition and is nondiffusable. Preferred methods of binding include the use of antibodies (which do not sterically block either the ligand binding site or activation sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein or other innocuous protein or other moiety.

In a preferred embodiment, the angiogenesis protein is bound to the support, and a candidate bioactive agent is added to the assay. Alternatively, the candidate agent is bound to the support and the angiogenesis protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled in vitro protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.) and the like.

The determination of the binding of the candidate bioactive agent to the angiogenesis protein may be done in a number of ways. In a preferred embodiment, the candidate bioactive agent is labelled, and binding determined directly. For example, this may be done by attaching all or a portion of the angiogenesis protein to a solid support, adding a labelled candidate agent (for example a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as is known in the art.

By "labeled" herein is meant that the compound is either directly or indirectly labeled with a label which provides a detectable signal, e.g. radioisotope, fluorescers, enzyme, antibodies, particles such as

magnetic particles, chemiluminescers, or specific binding molecules, etc. Specific binding molecules include pairs, such as biotin and streptavidin, digoxin and antidigoxin etc. For the specific binding members, the complementary member would normally be labeled with a molecule which provides for detection, in accordance with known procedures, as outlined above. The label can directly or indirectly provide a detectable signal.

In some embodiments, only one of the components is labeled. For example, the proteins (or proteinaceous candidate agents) may be labeled at tyrosine positions using ^{125}I, or with fluorophores. Alternatively, more than one component may be labeled with different labels; using ^{125}I for the proteins, for example, and a fluorophor for the candidate agents.

In a preferred embodiment, the binding of the candidate bioactive agent is determined through the use of competitive binding assays. In this embodiment, the competitor is a binding moiety known to bind to the target molecule (i.e. angiogenesis), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding as between the bioactive agent and the binding moiety, with the binding moiety displacing the bioactive agent.

In one embodiment, the candidate bioactive agent is labeled. Either the candidate bioactive agent, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at any temperature which facilitates optimal activity, typically between 4 and 40°C. Incubation periods are selected for optimum activity, but may also be optimized to facilitate rapid high through put screening. Typically between 0.1 and 1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

In a preferred embodiment, the competitor is added first, followed by the candidate bioactive agent. Displacement of the competitor is an indication that the candidate bioactive agent is binding to the angiogenesis protein and thus is capable of binding to, and potentially modulating, the activity of the angiogenesis protein. In this embodiment, either component can be labeled. Thus, for example, if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent. Alternatively, if the candidate bioactive agent is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the candidate bioactive agent is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the bioactive agent is bound to the angiogenesis protein with a higher affinity. Thus, if the candidate

bioactive agent is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the candidate agent is capable of binding to the angiogenesis protein.

In a preferred embodiment, the methods comprise differential screening to identity bioactive agents that are capable of modulating the activitity of the angiogenesis proteins. In this embodiment, the methods comprise combining an angiogenesis protein and a competitor in a first sample. A second sample comprises a candidate bioactive agent, an angiogenesis protein and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the angiogenesis protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the angiogenesis protein.

Alternatively, a preferred embodiment utilizes differential screening to identify drug candidates that bind to the native angiogenesis protein, but cannot bind to modified angiogenesis proteins. The structure of the angiogenesis protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect angiogenesis bioactivity are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

Positive controls and negative controls may be used in the assays. Preferably all control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples is for a time sufficient for the binding of the agent to the protein. Following incubation, all samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g. albumin, detergents, etc which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in any order that provides for the requisite binding.

Screening for agents that modulate the activity of angiogenesis proteins may also be done. In a preferred embodiment, methods for screening for a bioactive agent capable of modulating the activity of angiogenesis proteins comprise the steps of adding a candidate bioactive agent to a sample of angiogenesis proteins, as above, and determining an alteration in the biological activity of

angiogenesis proteins. "Modulating the activity of angiogenesis proteins" includes an increase in activity, a decrease in activity, or a change in the type or kind of activity present. Thus, in this embodiment, the candidate agent should both bind to angiogenesis proteins(although this may not be necessary), and alter its biological or biochemical activity as defined herein. The methods include both in vitro screening methods, as are generally outlined above, and in vivo screening of cells for alterations in the presence, distribution, activity or amount of angiogenesis proteins.

Thus, in this embodiment, the methods comprise combining an angiogenesis sample and a candidate bioactive agent, and evaluating the effect on angiogenesis. By "angiogenesis activity" or grammatical equivalents herein is meant one of angiogenesis's biological activities, including, but not limited to, its role in angiogenesis. In one embodiment, angiogenesis activity includes activation of AAA4, AAA1, Edg-1, alpha 5 beta1 integrin, endomucin and matrix metalloproteinase 10. An inhibitor of angiogenesis activity is the inhibition of any one or more angiogenesis activities.

In a preferred embodiment, the activity of the angiogenesis protein is increased; in another preferred embodiment, the activity of the angiogenesis protein is decreased. Thus, bioactive agents that are antagonists are preferred in some embodiments, and bioactive agents that are agonists may be preferred in other embodiments.

In a preferred embodiment, the invention provides methods for screening for bioactive agents capable of modulating the activity of an angiogenesis protein. The methods comprise adding a candidate bioactive agent, as defined above, to a cell comprising angiogenesis proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes an angiogenesis protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, for example hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including chemotherapeutics, radiation, carcinogenics, or other cells (i.e. cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

In this way, bioactive agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the angiogenesis protein. In one embodiment, "angiogenesis protein activity" as used herein includes at least one of the following: angiogenesis protein activity as defined herein, binding to Edg-1, activation of Edg-1, or activation of substrates of Edg-1. In one embodiment, angiogenesis activity is defined as the unregulated proliferation of angiogenic tissue, or

the growth of arteries in tissue. In one aspect, angiogenesis activity as defined herein is related to the activity of Edg-1 in the upregulation of Edg-1 in angiogenic tissue.

In another embodiment, angiogenesis protein activity includes at least one of the following: angiogenesis activity, binding to one of AAA4, AAA1, Edg-1, alpha 5 beta 1 integrin, endomucin, matrix metalloproteinase 10, or activation of substrates of AAA4, AAA1, Edg-1, alpha 5 beta 1 integrin, endomucin, matrix metalloproteinase 10, respectively. In one preferred embodiment, AAA1 comprises its N-terminal end. In one aspect, angiogenesis activity as defined herein is related to the activity of AAA4, AAA1, Edg-1, alpha 5 beta 1 integrin, endomucin, matrix metalloproteinase 10, in the upregulation of AAA4, AAA1, Edg-1, alpha 5 beta 1 integrin, endomucin, matrix metalloproteinase 10, respectively in angiogenesis tissue.

In one embodiment, a method of inhibiting angiogenic cell division is provided. The method comprises administration of a angiogenesis inhibitor.

In another embodiment, a method of inhibiting angiogenesis is provided. The method comprises administration of an angiogenesis inhibitor.

In a further embodiment, methods of treating cells or individuals with angiogenesis are provided. The method comprises administration of an angiogenesis inhibitor.

In one embodiment, an angiogenesis inhibitor is an antibody as discussed above. In another embodiment, the angiogenesis inhibitor is an antisense molecule. Antisense molecules as used herein include antisense or sense oligonucleotides comprising a singe-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for angiogenesis molecules. A preferred antisense molecule is for AAA4, AAA1, Edg-1, alpha 5 beta 1 integrin, endomucin, or matrix metalloproteinase 10, more preferable the angiogenesis sequences in Table 5, or for a ligand or activator thereof. A most preferred antisense molecule is for Edg-1 or for a ligand or activator thereof. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, for example, Stein and Cohen (Cancer Res. 48:2659, 1988) and van der Krol et al. (BioTechniques 6:958, 1988).

Antisense molecules may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable

ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a sense or an antisense oligonucleotide may be introduced into a cell containing the target nucleic acid sequence by formation of an oligonucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

The compounds having the desired pharmacological activity may be administered in a physiologically acceptable carrier to a host, as previously described. The agents may be administered in a variety of ways, orally, parenterally e.g., subcutaneously, intraperitoneally, intravascularly, etc. Depending upon the manner of introduction, the compounds may be formulated in a variety of ways. The concentration of therapeutically active compound in the formulation may vary from about 0.1-100 wt.%. The agents may be administered alone or in combination with other treatments, i.e., radiation.

The pharmaceutical compositions can be prepared in various forms, such as granules, tablets, pills, suppositories, capsules, suspensions, salves, lotions and the like. Pharmaceutical grade organic or inorganic carriers and/or diluents suitable for oral and topical use can be used to make up compositions containing the therapeutically-active compounds. Diluents known to the art include aqueous media, vegetable and animal oils and fats. Stabilizing agents, wetting and emulsifying agents, salts for varying the osmotic pressure or buffers for securing an adequate pH value, and skin penetration enhancers can be used as auxiliary agents.

Without being bound by theory, it appears that the various angiogenesis sequences are important in angiogenesis. Accordingly, disorders based on mutant or variant angiogenesis genes may be determined. In one embodiment, the invention provides methods for identifying cells containing variant angiogenesis genes comprising determining all or part of the sequence of at least one endogeneous angiogenesis genes in a cell. As will be appreciated by those in the art, this may be done using any number of sequencing techniques. In a preferred embodiment, the invention provides methods of identifying the angiogenesis genotype of an individual comprising determining all or part of the sequence of at least one angiogenesis gene of the individual. This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced angiogenesis gene to a known angiogenesis gene, i.e. a wild-type gene.

The sequence of all or part of the angiogenesis gene can then be compared to the sequence of a known angiogenesis gene to determine if any differences exist. This can be done using any number of known homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a a difference in the sequence between the angiogenesis gene of the patient and the known angiogenesis gene is indicative of a disease state or a propensity for a disease state, as outlined herein.

In a preferred embodiment, the angiogenesis genes are used as probes to determine the number of copies of the angiogenesis gene in the genome.

In another preferred embodiment, the angiogenesis genes are used as probes to determine the chromosomal localization of the angiogenesis genes. Information such as chromosomal localization finds use in providing a diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in the angiogenesis gene locus.

Thus, in one embodiment, methods of modulating angiogenesis in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-angiogenesis antibody that reduces or eliminates the biological activity of an endogeneous angiogenesis protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic acid encoding an angiogenesis protein. As will be appreciated by those in the art, this may be accomplished in any number of ways. In a preferred embodiment, for example when the angiogenesis sequence is down-regulated in angiogenesis, the activity of the angiogenesis gene is increased by increasing the amount of angiogenesis in the cell, for example by overexpressing the endogeneous angiogenesis or by administering a gene encoding the angiogenesis sequence, using known gene-therapy techniques, for example. In a preferred embodiment, the gene therapy techniques include the incorporation of the exogenous gene using enhanced homologous recombination (EHR), for example as described in PCT/US93/03868, hereby incorporated by reference in its entireity. Alternatively, for example when the angiogenesis sequence is up-regulated in angiogenesis, the activity of the endogeneous angiogenesis gene is decreased, for example by the administration of a angiogenesis antisense nucleic acid.

In one embodiment, the angiogenesis proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to angiogenesis proteins, which are useful as described herein. Similarly, the angiogenesis proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify angiogenesis antibodies. In a preferred embodiment, the antibodies are generated to epitopes unique to a angiogenesis protein; that is, the antibodies show little or no cross-reactivity to other proteins. These antibodies find use in a

number of applications. For example, the angiogenesis antibodies may be coupled to standard affinity chromatography columns and used to purify angiogenesis proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the angiogenesis protein.

In one embodiment, a therapeutically effective dose of an angiogenesis proteins and modulator thereof is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces the effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques. As is known in the art, adjustments for angiogenesis degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration, drug interaction and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals, and organisms. Thus the methods are applicable to both human therapy and veterinary applications. In the preferred embodiment the patient is a mammal, and in the most preferred embodiment the patient is human.

The administration of the angiogenesis proteins and modulators thereof of the present invention can be done in a variety of ways as discussed above, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly. In some instances, for example, in the treatment of wounds and inflammation, the angiogenesis proteins and modulators may be directly applied as a solution or spray.

The pharmaceutical compositions of the present invention comprise an angiogenesis protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as

sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose, lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol. Additives are well known in the art, and are used in a variety of formulations.

In a preferred embodiment, angiogenesis proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, angiogenesis genes (including both the full-length sequence, partial sequences, or regulatory sequences of the angiogenesis coding regions) can be administered in gene therapy applications, as is known in the art. These angiogenesis genes can include antisense applications, either as gene therapy (i.e. for incorporation into the genome) or as antisense compositions, as will be appreciated by those in the art.

In a preferred embodiment, angiogenesis genes are administered as DNA vaccines, either single genes or combinations of angiogenesis genes. Naked DNA vaccines are generally known in the art. Brower, Nature Biotechnology, 16:1304-1305 (1998).

In one embodiment, angiogenesis genes of the present invention are used as DNA vaccines. Methods for the use of genes as DNA vaccines are well known to one of ordinary skill in the art, and include placing an angiogenesis gene or portion of an angiogenesis gene under the control of a promoter for expression in an angiogenesis patient. The angiogenesis gene used for DNA vaccines can encode full-length angiogenesis proteins, but more preferably encodes portions of the angiogenesis proteins including peptides derived from the angiogenesis protein. In a preferred embodiment a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from an angiogenesis gene. Similarly, it is possible to immunize a patient with a plurality of angiogenesis genes or portions thereof as defined herein. Without being bound by theory, expression of the polypeptide encoded by the DNA vaccine, cytotoxic T-cells, helper T-cells and antibodies are induced which recognize and destroy or eliminate cells expressing angiogenesis proteins.

In a preferred embodiment, the DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the angiogenesis polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are known to those of ordinary skill in the art and find use in the invention.

In another preferred embodiment angiogenesis genes find use in generating animal models of angiogenesis. As is appreciated by one of ordinary skill in the art, when the angiogenesis gene identified is repressed or diminished in angiogenesis tissue, gene therapy technology wherein antisense RNA directed to the angiogenesis gene will also diminish or repress expression of the gene. An animal generated as such serves as an animal model of angiogenesis that finds use in screening bioactive drug candidates. Similarly, gene knockout technology, for example as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence of the angiogenesis protein. When desired, tissue-specific expression or knockout of the angiogenesis protein may be necessary.

It is also possible that the angiogenesis protein is overexpressed in angiogenesis. As such, transgenic animals can be generated that overexpress the angiogenesis protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene. Animals generated by such methods find use as animal models of angiogenesis and are additionally useful in screening for bioactive molecules to treat angiogenesis.

It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All references and sequences of accession numbers cited herein are incorporated by reference in their entirety.

EXAMPLES

Example 1

Tissue Preparation, Labeling Chips, and Fingerprints

Purify total RNA from tissue using TRIzol Reagent

Estimate tissue weight. Homogenize tissue samples in 1ml of TRIzol per 50mg of tissue using a Polytron 3100 homogenizer. The generator/probe used depends upon the tissue size. A

generator that is too large for the amount of tissue to be homogenized will cause a loss of sample and lower RNA yield. Use the 20mm generator for tissue weighing more than 0.6g. If the working volume is greater than 2ml, then homogenize tissue in a 15ml polypropylene tube (Falcon 2059). Fill tube no greater than 10ml.

HOMOGENIZATION

Before using generator, it should have been cleaned after last usage by running it through soapy H20 and rinsing thoroughly. Run through with EtOH to sterilize. Keep tissue frozen until ready. Add TRIzol directly to frozen tissue then homogenize.

Following homogenization, remove insoluble material from the homogenate by centrifugation at 7500 x g for 15 min. in a Sorvall superspeed or 12,000 x g for 10 min. in an Eppendorf centrifuge at 4°C. Transfer the cleared homogenate to a new tube(s). The samples may be frozen now at -60 to -70°C (and kept for at least one month) or you may continue with the purification.

PHASE SEPARATION

Incubate the homogenized samples for 5 minutes at room temperature.
Add 0.2ml of chloroform per 1ml of TRIzol reagent used in the original homogenization.
Cap tubes securely and shake tubes vigorously by hand (do not vortex) for 15 seconds.
Incubate samples at room temp. for 2-3 minutes. Centrifuge samples at 6500rpm in a Sorvall superspeed for 30 min. at 4°C. (You may spin at up to 12,000 x g for 10 min. but you risk breaking your tubes in the centrifuge.)

RNA PRECIPITATION

Transfer the aqueous phase to a fresh tube. Save the organic phase if isolation of DNA or protein is desired. Add 0.5ml of isopropyl alcohol per 1ml of TRIzol reagent used in the original homogenization. Cap tubes securely and invert to mix. Incubate samples at room temp. for 10 minutes. Centrifuge samples at 6500rpm in Sorvall for 20min. at 4°C.

RNA WASH

Pour off the supernate. Wash pellet with cold 75% ethanol. Use 1ml of 75% ethanol per 1ml of TRIzol reagent used in the initial homogenization. Cap tubes securely and invert several times to loosen pellet. (Do not vortex). Centrifuge at <8000rpm (<7500 x g) for 5 minutes at 4°C.
Pour off the wash. Carefully transfer pellet to an eppendorf tube (let it slide down the tube into the new tube and use a pipet tip to help guide it in if necessary). Depending on the volumes you are working with, you can decide what size tube(s) you want to precipitate the RNA in. When I tried

leaving the RNA in the large 15ml tube, it took so long to dry (i.e. it did not dry) that I eventually had to transfer it to a smaller tube. Let pellet dry in hood. Resuspend RNA in an appropriate volume of DEPC H_20. Try for 2-5ug/ul. Take absorbance readings.

Purify poly A+ mRNA from total RNA or clean up total RNA with Qiagen' s RNeasy kit

Purification of poly A$^+$ mRNA from total RNA. Heat oligotex suspension to 37°C and mix immediately before adding to RNA. Incubate Elution Buffer at 70°C. Warm up 2 x Binding Buffer at 65°C if there is precipitate in the buffer. Mix total RNA with DEPC-treated water, 2 x Binding Buffer, and Oligotex according to Table 2 on page 16 of the Oligotex Handbook. Incubate for 3 minutes at 65°C. Incubate for 10 minutes at room temperature.

Centrifuge for 2 minutes at 14,000 to 18,000 g. If centrifuge has a "soft setting," then use it. Remove supernatant without disturbing Oligotex pellet. A little bit of solution can be left behind to reduce the loss of Oligotex. Save sup until certain that satisfactory binding and elution of poly A$^+$ mRNA has occurred.

Gently resuspend in Wash Buffer OW2 and pipet onto spin column. Centrifuge the spin column at full speed (soft setting if possible) for 1 minute.

Transfer spin column to a new collection tube and gently resuspend in Wash Buffer OW2 and centrifuge as describe herein.

Transfer spin column to a new tube and elute with 20 to 100 ul of preheated (70°C) Elution Buffer. Gently resuspend Oligotex resin by pipetting up and down. Centrifuge as above. Repeat elution with fresh elution buffer or use first eluate to keep the elution volume low.

Read absorbance, using diluted Elution Buffer as the blank.

Before proceeding with cDNA synthesis, the mRNA must be precipitated.
Some component leftover or in the Elution Buffer from the Oligotex purification procedure will inhibit downstream enzymatic reactions of the mRNA.

Ethanol Precipitation

Add 0.4 vol. of 7.5 M NH_4OAc + 2.5 vol. of cold 100% ethanol. Precipitate at -20°C 1 hour to overnight (or 20-30 min. at -70°C). Centrifuge at 14,000-16,000 x g for 30 minutes at 4°C. Wash

pellet with 0.5ml of 80%ethanol (-20°C) then centrifuge at 14,000-16,000 x g for 5 minutes at room temperature. Repeat 80% ethanol wash. Dry the last bit of ethanol from the pellet in the hood. (Do not speed vacuum). Suspend pellet in DEPC H_20 at 1ug/ul concentration.

Clean up total RNA using Qiagen's RNeasy kit

Add no more than 100ug to an RNeasy column. Adjust sample to a volume of 100ul with RNase-free water. Add 350ul Buffer RLT then 250ul ethanol (100%) to the sample. Mix by pipetting (do not centrifuge) then apply sample to an RNeasy mini spin column. Centrifuge for 15 sec at >10,000rpm. If concerned about yield, re-apply flowthrough to column and centrifuge again. Transfer column to a new 2-ml collection tube. Add 500ul Buffer RPE and centrifuge for 15 sec at >10,000rpm. Discard flowthrough. Add 500ul Buffer RPE and centrifuge for 15 sec at >10,000rpm. Discard flowthrough then centrifuge for 2 min at maximum speed to dry column membrane. Transfer column to a new 1.5-ml collection tube and apply 30-50ul of RNase-free water directly onto column membrane. Centrifuge 1 min at >10,000rpm. Repeat elution. Take absorbance reading. If necessary, ethanol precipitate with ammonium acetate and 2.5X volume 100% ethanol.

Make cDNA using Gibco's "SuperScript Choice System for cDNA Synthesis" kit

First Strand cDNA Synthesis

Use 5ug of total RNA or 1ug of polyA+ mRNA as starting material. For total RNA, use 2ul of SuperScript RT. For polyA+ mRNA, use 1ul of SuperScript RT. Final volume of first strand synthesis mix is 20ul. RNA must be in a volume no greater than 10ul. Incubate RNA with 1ul of 100pmol T7-T24 oligo for 10 min at 70C. On ice, add 7 ul of: 4ul 5X 1st Strand Buffer, 2ul of 0.1M DTT, and 1 ul of 10mM dNTP mix. Incubate at 37C for 2 min then add SuperScript RT Incubate at 37C for 1 hour.

Second Strand Synthesis

Place 1st strand reactions on ice.

Add: 91ul DEPC H20
30ul 5X 2nd Strand Buffer
3ul 10mM dNTP mix
1ul 10U/ul *E.coli* DNA Ligase
4ul 10U/ul *E.coli* DNA Polymerase
1ul 2U/ul RNase H

Make the above into a mix if there are more than 2 samples. Mix and incubate 2 hours at 16C.

Add 2ul T4 DNA Polymerase. Incubate 5 min at 16C. Add 10ul of 0.5M EDTA

Clean up cDNA

Phenol:Chloroform:Isoamyl Alcohol (25:24:1) purification using Phase-Lock gel tubes: Centrifuge PLG tubes for 30 sec at maximum speed. Transfer cDNA mix to PLG tube. Add equal volume of phenol:chloroform:isamyl alcohol and shake vigorously (do not vortex). Centrifuge 5 minutes at maximum speed. Transfer top aqueous solution to a new tube. Ethanol precipitate: add 7.5X 5M NH4Oac and 2.5X volume of 100% ethanol. Centrifuge immediately at room temp. for 20 min, maximum speed. Remove sup then wash pellet 2X with cold 80% ethanol. Remove as much ethanol wash as possible then let pellet air dry. Resuspend pellet in 3ul RNase-free water.

In vitro Transcription (IVT) and labeling with biotin

Pipet 1.5ul of cDNA into a thin-wall PCR tube.

Make NTP labeling mix:

Combine at room temperature:	2ul	T7 10xATP (75mM) (Ambion)
	2ul	T7 10xGTP (75mM) (Ambion)
	1.5ul	T7 10xCTP (75mM) (Ambion)
	1.5ul	T7 10xUTP (75mM) (Ambion)
	3.75ul	10mM Bio-11-UTP (Boehringer-Mannheim/Roche or Enzo)
	3.75ul	10mM Bio-16-CTP (Enzo)
	2ul	10x T7 transcription buffer (Ambion)
	2ul	10x T7 enzyme mix (Ambion)

Final volume of total reaction is 20ul. Incubate 6 hours at 37C in a PCR machine.

RNeasy clean-up of IVT product

Follow previous instructions for RNeasy columns or refer to Qiagen's RNeasy protocol handbook.

cRNA will most likely need to be ethanol precipitated. Resuspend in a volume compatible with the fragmentation step.

Fragmentation

15 ug of labeled RNA is usually fragmented. Try to minimize the fragmentation reaction volume; a 10 ul volume is recommended but 20 ul is all right. Do not go higher than 20 ul because the magnesium in the fragmentation buffer contributes to precipitation in the hybridization buffer. Fragment RNA by incubation at 94 C for 35 minutes in 1 x Fragmentation buffer.

5 x Fragmentation buffer:
200 mM Tris-acetate, pH 8.1
500 mM KOAc
150 mM MgOAc

The labeled RNA transcript can be analyzed before and after fragmentation. Samples can be heated to 65C for 15 minutes and electrophoresed on 1% agarose/TBE gels to get an approximate idea of the transcript size range

Hybridization

200 ul (10ug cRNA) of a hybridization mix is put on the chip. If multiple hybridizations are to be done (such as cycling through a 5 chip set), then it is recommended that an initial hybridization mix of 300 ul or more be made.

Hybrization Mix: fragment labeled RNA (50ng/ul final conc.)
50 pM 948-b control oligo
1.5 pM BioB
5 pM BioC
25 pM BioD
100 pM CRE
0.1mg/ml herring sperm DNA
0.5mg/ml acetylated BSA
to 300 ul with 1xMES hyb. buffer

The instruction manuals for the products used herein are incorporated herein in their entirety.

Labeling Protocol Provided Herein

Hybridization reaction:
Start with non-biotinylated IVT (purified by RNeasy columns)
(see example 1 for steps from tissue to IVT)
IVT antisense RNA; 4 µg: µl

Random Hexamers (1 µg/µl): 4 µl
H_2O: µl

14 µl

- Incubate 70°C, 10 min. Put on ice.

Reverse transcription:
5X First Strand (BRL) buffer: 6 µl
0.1 M DTT: 3 µl
50X dNTP mix: 0.6 µl
H2O: 2.4 µl
Cy3 or Cy5 dUTP (1mM): 3 µl
SS RT II (BRL): 1 µl

16 µl

- Add to hybridization reaction.
- Incubate 30 min., 42°C.
- Add 1 µl SSII and let go for another hour.
Put on ice.
- 50X dNTP mix (25mM of cold dATP, dCTP, and dGTP, 10mM of dTTP: 25 µl each of 100mM dATP, dCTP, and dGTP; 10 µl of 100mM dTTP to 15 µl H2O. dNTPs from Pharmacia)

RNA degradation:

86 µl H_2O
- Add 1.5 µl 1M NaOH/ 2mM EDTA, incubate at 65°C, 10 min. 10 µl 10N NaOH
4 µl 50mM EDTA

U-Con 30
500 µl TE/sample spin at 7000g for 10 min, save flow through for purification

Qiagen purification:
-suspend u-con recovered material in 500µl buffer PB
-proceed w/ normal Qiagen protocol
DNAse digest:
- Add 1 µl of 1/100 dil of DNAse/30µl Rx and incubate at 37°C for 15 min.
-5 min 95°C to denature enzyme

Sample preparation:

- Add:

Cot-1 DNA: 10 µl	
50X dNTPs: 1 µl	
20X SSC: 2.3 µl	
Na pyro phosphate: 7.5 µl	
10mg/ml Herring sperm DNA	1ul of 1/10 dilution
	21.8 final vol.

- Dry down in speed vac.
- Resuspend in 15 µl H_2O.
- Add 0.38 µl 10% SDS.
- Heat 95°C, 2 min.
- Slow cool at room temp. for 20 min.

Put on slide and hybridize overnight at 64°C.

Washing after the hybridization:

3X SSC/0.03% SDS:	2 min. 37.5 mls 20X SSC+0.75mls 10% SDS in 250mls H_2O
1X SSC: 5 min.	12.5 mls 20X SSC in 250mls H_2O
0.2X SSC: 5 min.	2.5 mls 20X SSC in 250mls H_2O

Dry slides in centrifuge, 1000 RPM, 1min.

Scan at appropiate PMT's and channels.

The results are shown in the tables and figures. The lists of genes come from cells cultured in an in vitro angiogenesis model. As indicated, some of the Accession numbers include expression sequence tags (ESTs). Thus, in one embodiment herein, genes within an expression profile, also termed expression profile genes, include ESTs and are not necessarily full length.

TABLE 1

Cluster	Accession # / PROBESET	Gene Description
3	AB000450	vaccinia related kinase 2
4	AB002380	Human mRNA for KIAA382 gene; partial cds
4	AB003103	proteasome (prosome; macropain) 26S subunit; non-ATPase; 12
4	AB004884	Homo sapiens mRNA for PKU-alpha; partial cds
1	AF000573_ma1	homogentisate 1;2-dioxygenase (homogentisate oxidase)
3	AF008937	Homo sapiens syntaxin-16C mRNA, complete cds
3	AF009301	Homo sapiens TEB4 protein mRNA; complete cds
3	AF009368	Homo sapiens Luman mRNA; complete cds
4	D00591	chromosome condensation 1
4	D00760	proteasome (prosome; macropain) subunit; alpha type; 2
1	D11139	tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity; collagenase inhibitor)
4	D14657	Human mRNA for KIAA11 gene; complete cds
4	D14878	D123 gene product
1	D17716	mannosyl (alpha-1;6-)-glycoprotein beta-1;6-N-acetyl-glucosaminyltransferase
4	D21090	RAD23 (S. cerevisiae) homolog B
1	D26135	diacylglycerol kinase; gamma (9kD)
1	D26528	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 7 (RNA helicase; 52kD)
1	D30742	calcium/calmodulin-dependent protein kinase IV
4	D31762	Human mRNA for KIAA57 gene; complete cds
4	D31765	Human mRNA for KIAA61 gene; partial cds
3	D31888	Homo sapiens clone 2479 mRNA sequence
4	D38128	prostaglandin I2 (prostacyclin) receptor (IP)
2	D38500	postmeiotic segregation increased 2-like 4
4	D38551	RAD21 (S. pombe) homolog
4	D42087	Human mRNA for KIAA118 gene; partial cds
3	D49396	Human mRNA for Apo1_Human (MER5(Aop1-Mouse)-like protein); complete cds
4	D55640	Human monocyte PABL (pseudoautosomal boundary-like sequence) mRNA, clone Mo2
1	D63391	platelet-activating factor acetylhydrolase; isoform Ib; gamma subunit (29kD)
3	D63477	Human mRNA for KIAA143 gene; partial cds
4	D63483	acetyl LDL receptor; SREC
4	D64015	TIA1 cytotoxic granule-associated RNA-binding protein-like 1
4	D79990	Human mRNA for KIAA168 gene; complete cds
4	D79997	Human mRNA for KIAA175 gene; complete cds
4	D80010	Human mRNA for KIAA188 gene; partial cds
1	D84276	CD38 antigen (p45)
4	D86425	Homo sapiens mRNA for nidogen-2
4	D86978	Human mRNA for KIAA225 gene; partial cds

Cluster	Accession # / PROBESET	Gene Description
1	D87012	Homo sapiens clone 24675 mRNA sequence
4	D87075	Human mRNA for KIAA238 gene; partial cds
4	D87432	solute carrier family 7 (cationic amino acid transporter; y+ system);
4	D87448	Homo sapiens mRNA for DNA topoisomerase II binding protein; complete cds
2	D87845	platelet-activating factor acetylhydrolase 2 (4kD)
1	HG1098-HT1098	Cystatin D
4	HG2167-HT2237	Protein Kinase Ht31, Camp-Dependent
1	HG2415-HT2511	Transcription Factor E2f-2
1	HG2825-HT2949	Ret Transforming Gene
1	HG2887-HT3031_r	Sry-Related Hmg-Box 12 Protein (Gb:X73039)
4	HG4660-HT5073	Microtubule-Associated Protein 1b
3	HG4704-HT5146	Glial Growth Factor 2
4	HG884-HT884	Oncogene E6-Ap, Papillomavirus
1	HG919-HT919	Dna Polymerase, Epsilon, Catalytic Subunit
4	J00212_f	Accession not listed in Genbank
4	J04029	keratin 1 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris)
4	J04031	5;1-methylenetetrahydrofolate dehydrogenase; 5;1-methylenetetrahydrofolate cyclohydrolase; 1-formyltetrahydrofolate synthetase
4	J04088	topoisomerase (DNA) II alpha (17kD)
4	J04543	annexin VII (synexin)
4	L06139	TEK tyrosine kinase; endothelial
1	L07540	ACTIVATOR 1 36 KD SUBUNIT
4	L08895	MADS box transcription enhancer factor 2; polypeptide C (myocyte enhancer factor 2C)
1	L11239	gastrulation brain homeo box 1
1	L11353	neurofibromin 2 (bilateral acoustic neuroma)
4	L13773	Human AF-4 mRNA; complete cds
4	L13800	Homo sapiens liver expressed protein gene, 3' end
4	L14922	replication factor C (activator 1) 1 (145kD)
4	L15189	heat shock 7kD protein 9B (mortalin-2)
4	L15388	Human G protein-coupled receptor kinase (GRK5) mRNA, complete cds
3	L16895	lysyl oxidase
4	L27476	Friedreich ataxia region gene X14 (tight junction protein ZO-2)
4	L27624	TISSUE FACTOR PATHWAY INHIBITOR 2 PRECURSOR
1	L32976	mixed lineage kinase 3
1	L33404	protease; serine; 6 (chymotryptic; stratum corneum)
4	L35263	cytokine suppressive anti-inflammatory drug binding protein 1 (p38 MAP kinase)
1	L37347	natural resistance-associated macrophage protein 2
4	L40371	thyroid hormone receptor interactor 4
4	L40391	Homo sapiens (clone s153) mRNA fragment

Cluster	Accession # / PROBESET	Gene Description
4	L41607	glucosaminyl (N-acetyl) transferase 2; I-branching enzyme
1	L77566	Homo sapiens DGS-I mRNA; 3' end
1	M13928	aminolevulinate; delta-; dehydratase
1	M14016	uroporphyrinogen decarboxylase
4	M14219	decorin
4	M15796	proliferating cell nuclear antigen
4	M21305	Human alpha satellite and satellite 3 junction DNA sequence
4	M22092	Human neural cell adhesion molecule (N-CAM) gene, exon SEC and partial cds
4	M22898	tumor protein p53 (Li-Fraumeni syndrome)
3	M22995	RAP1A; member of RAS oncogene family
3	M23379	RAS p21 protein activator (GTPase activating protein) 1
1	M24364	major histocompatibility complex; class II; DQ beta 1
1	M24400	chymotrypsinogen B1
3	M25753	cyclin B1
4	M27691	cAMP responsive element binding protein 1
4	M28213	RAB2; member RAS oncogene family
4	M29550	SERINE/THREONINE PROTEIN PHOSPHATASE 2B CATALYTIC SUBUNIT; BETA ISOFORM
1	M29971	O-6-methylguanine-DNA methyltransferase
4	M30269	nidogen (enactin)
4	M31158	protein kinase; cAMP-dependent; regulatory; type II; beta
3	M31166	pentaxin-related gene; rapidly induced by IL-1 beta
3	M31210	endothelial differentiation; sphingolipid G-protein-coupled receptor; 1
1	M55420	Human IgE chain, last 2 exons
4	M59979	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)
4	M62810	transcription factor 6-like 1 (mitochondrial transcription factor 1-like)
4	M63838	interferon; gamma-inducible protein 16
1	M64710	Human C-type natriuretic peptide gene, complete cds
3	M68874	Human phosphatidylcholine 2-acylhydrolase (cPLA2) mRNA, complete cds
3	M74524	ubiquitin-conjugating enzyme E2A (RAD6 homolog)
1	M80254	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE; MITOCHONDRIAL PRECURSOR
1	M81780_cds3	sphingomyelin phosphodiesterase 1; acid lysosomal (acid sphingomyelinase)
4	M83822	Human beige-like protein (BGL) mRNA; partial cds
4	M86934	GS1 PROTEIN
1	M87338	replication factor C (activator 1) 2 (4kD)
1	M96326_ma1	azurocidin 1 (cationic antimicrobial protein 37)
4	M96954	TIA1 cytotoxic granule-associated RNA-binding protein-like 1
4	M98833	Friend leukemia virus integration 1
1	S66793	arrestin 3; retinal (X-arrestin)

Cluster	Accession # / PROBESET	Gene Description
1	S72370	pyruvate carboxylase
4	S78569	laminin; alpha 4
4	S79873	lysosomal-associated membrane protein 2
1	S83325	aspartate beta-hydroxylase
4	S83364	putative Rab5-interacting protein (clone L1-57) [human, HeLa cells, mRNA Partial, 366 nt]
1	S83365	putative Rab5-interacting protein (clone L1-94) [human, HeLa cells, mRNA Partial, 369 nt]
1	U01212	Human olfactory marker protein (OMP) gene, complete cds
1	U01922	deafness; X-linked 1; progressive
4	U02556	Human RP3 mRNA; complete cds
4	U02680	protein tyrosine kinase 9
4	U03272	fibrillin 2
4	U04209	Human associated microfibrillar protein mRNA; complete cds
4	U05237	fetal Alzheimer antigen
1	U07225	purinergic receptor P2Y; G-protein coupled; 2
3	U07620	protein kinase mitogen-activated 1 (MAP kinase)
4	U09759	protein kinase mitogen-activated 9 (MAP kinase)
4	U09820	alpha thalassemia/mental retardation syndrome X-linked
3	U11313	sterol carrier protein 2
3	U14518	centromere protein A (17kD)
4	U14575	protein phosphatase 1; regulatory (inhibitor) subunit 8
3	U15173	BCL2/adenovirus E1B 19kD-interacting protein 2
4	U15932	dual specificity phosphatase 5
4	U18291	cell division cycle 16; anaphase promoting complex 6
4	U18300	damage-specific DNA binding protein 2 (48kD)
4	U18383	nuclear respiratory factor 1
4	U20536	caspase 6; apoptosis-related cysteine protease
4	U21551	Human ECA39 mRNA; complete cds
4	U23028	eukaryotic translation initiation factor 2B; subunit 5 (epsilon; 82kD)
1	U23752	SRY (sex-determining region Y)-box 11
4	U25435	Human transcriptional repressor (CTCF) mRNA; complete cds
4	U25997	stanniocalcin
4	U28251_cds2	zinc finger protein 169
4	U28831	Human protein immuno-reactive with anti-PTH polyclonal antibodies mRNA; partial cds
4	U30245	Human myelomonocytic specific protein (MNDA) gene, 5' flanking sequence and complete exon 1
4	U32315	Human syntaxin 3 mRNA; complete cds
4	U32439	regulator of G-protein signalling 7
3	U32849	N-myc (and STAT) interactor
4	U35139	necdin (mouse) homolog
1	U36764	eukaryotic translation initiation factor 3; subunit 2 (beta; 36kD)
4	U39400	chromosome 11 open reading frame 4
4	U39657	protein kinase; mitogen-activated; kinase 6 (MAP kinase kinase 6)

Cluster	Accession # / PROBESET	Gene Description
4	U41344	proline arginine-rich end leucine-rich repeat protein
3	U41766	a disintegrin and metalloproteinase domain 9 (meltrin gamma)
3	U41813	homeo box A9
3	U41815	Human nucleoporin 98 (NUP98) mRNA, complete cds
4	U43286	Human selenophosphate synthetase 2 (SPS2) mRNA; complete cds
4	U44378	MAD (mothers against decapentaplegic; Drosophila) homolog 4
4	U44754	small nuclear RNA activating complex; polypeptide 1; 43kD
1	U47011_cds1	fibroblast growth factor 8 (androgen-induced)
4	U47077	Human DNA-dependent protein kinase catalytic subunit (DNA-PKcs) mRNA; complete cds
4	U48251	Homo sapiens protein kinase C-binding protein RACK7 mRNA; partial cds
4	U50535	Human BRCA2 region; mRNA sequence CG6
4	U56833	von Hippel-Lindau binding protein 1
4	U58091	cullin 4B
1	U58837	cyclic nucleotide gated channel beta 1
4	U59289	cadherin 13; H-cadherin (heart)
4	U59863	TNF receptor-associated factor 2
4	U67122	ubiquitin-like 1 (sentrin)
4	U67319	caspase 7; apoptosis-related cysteine protease
3	U68019	MAD (mothers against decapentaplegic; Drosophila) homolog 3
1	U69611	a disintegrin and metalloproteinase domain 17 (tumor necrosis factor; alpha; converting enzyme)
4	U70322	karyopherin (importin) beta 2
4	U73524	Human putative ATP/GTP-binding protein (HEAB) mRNA; complete cds
4	U79267	Human clone 2384 mRNA; partial cds
4	U79291	Human clone 23721 mRNA sequence
4	U82671_cds2	Homo sapiens clone LM1955 H15e3 gene; partial cds
4	U84573	procollagen-lysine; 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2
4	U90914	carboxypeptidase D
1	U91316	Homo sapiens mRNA for brain acyl-CoA hydrolase; complete cds
4	U91932	clathrin-associated/assembly/adaptor protein; small 3; 22-kD; Sigma3A
4	U96131	Homo sapiens HPV16 E1 protein binding protein mRNA; complete cds
4	U97018	echinoderm microtubule-associated protein-like
4	U97188	Homo sapiens putative RNA binding protein KOC (koc) mRNA; complete cds
4	V00503	collagen; type I; alpha 2
3	X04327	2;3-bisphosphoglycerate mutase
1	X06389	synaptophysin
1	X07496	apolipoprotein A-I
2	X07820	matrix metalloproteinase 1 (stromelysin 2)
3	X14787	thrombospondin 1

Cluster	Accession # / PROBESET	Gene Description
4	X15525_ma1	acid phosphatase 2; lysosomal
3	X16396	NAD-DEPENDENT METHYLENETETRAHYDROFOLATE DEHYDROGENASE
4	X16609	ankyrin 1; erythrocytic
4	X53586_ma1	Human mRNA for integrin alpha 6
4	X53793	MULTIFUNCTIONAL PROTEIN ADE2
1	X54936	placental growth factor; vascular endothelial growth factor-related protein
4	X55740	5' nucleotidase (CD73)
2	X57025	insulin-like growth factor 1 (somatomedin C)
2	X60673_ma1	adenylate kinase 3
4	X60708	dipeptidylpeptidase IV (CD26; adenosine deaminase complexing protein 2)
4	X62048	wee1+ (S. pombe) homolog
2	X63097	Rhesus blood group; D antigen
4	X63563	polymerase (RNA) II (DNA directed) polypeptide B (14kD)
4	X64037	general transcription factor IIF; polypeptide 1 (74kD subunit)
4	X69636	hect domain and RLD 2
4	X69878	fms-related tyrosine kinase 4
4	X70649	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1
3	X72841	H.sapiens IEF 7442 mRNA
4	X74987	ribonuclease L (2';5'-oligoisoadenylate synthetase-dependent) inhibitor
4	X83107	BMX non-receptor tyrosine kinase
3	X84194	acylphosphatase 1; erythrocyte (common) type
4	X85753	cyclin-dependent kinase 8
1	X87870	H.sapiens mRNA for hepatocyte nuclear factor 4a
4	X89066	transient receptor potential channel 1
4	X89398_cds2	uracil-DNA glycosylase
1	X89399	Homo sapiens mRNA for Ins(1;3;4;5)P4-binding protein
3	X89426	H.sapiens mRNA for ESM-1 protein
4	X91247	thioredoxin reductase 1
4	X91648	H.sapiens mRNA for pur alpha extended 3'untranslated region
4	X92098	H.sapiens mRNA for transmembrane protein mp24
4	X92110	H.sapiens mRNA for hcgVIII protein
4	X94703	RAB28; member RAS oncogene family
1	X96506	H.sapiens mRNA for NC2 alpha subunit
1	X97230_f	Homo sapiens natural killer-associated transcript 5 (NKAT5) mRNA; complete cds
4	X98263	H.sapiens mRNA for M-phase phosphoprotein; mpp6
4	X98296	ubiquitin specific protease 9; X chromosome (Drosophila fat facets related)
4	X99584	H.sapiens mRNA for SMT3A protein

Cluster	Accession # / PROBESET	Gene Description
4	Y00264	amyloid beta (A4) precursor protein (protease nexin-II; Alzheimer disease)
4	Y07566	H.sapiens mRNA for RIT protein
3	Y07759	myosin VA (heavy polypeptide 12; myoxin)
1	Y07827	Human butyrophilin (BTF5) mRNA; complete cds
4	Y07867	pirin
4	Y09443	alkylglycerone phosphate synthase
4	Y09858	H.sapiens mRNA for unknown protein
4	Y12394	karyopherin alpha 3 (importin alpha 4)
3	Z11559	iron-responsive element binding protein 1
4	Z11695	protein kinase; mitogen-activated 1 (MAP kinase 1; p4; p41)
3	Z15005	centromere protein E (312kD)
1	Z46261	H.sapiens DNA for histone H3a
2	AA011243_s	ESTs
2	AA018418	ESTs
2	AA018758	ESTs
2	AA018804	Homo sapiens clone 23675 mRNA sequence
3	AA031993	Homo sapiens HRIHFB2115 mRNA; partial cds
2	AA044217	ESTs; Weakly similar to similar to cuticle collagen [C.elegans]
4	AA046548	SWI/SNF related; matrix associated; actin dependent regulator of chromatin; subfamily e; member 1
2	AA057447_s	ESTs; Moderately similar to !!!! ALU SUBFAMILY SB WARNING ENTRY !!!! [H.sapiens]
2	AA058376	Sjogren syndrome antigen A2 (6kD; ribonucleoprotein autoantigen SS-A/Ro)
4	AA083572	v-ral simian leukemia viral oncogene homolog A (ras related)
4	AA085696	ESTs
2	AA088744	ESTs
2	AA089688	ESTs; Weakly similar to putative T1/ST2 receptor binding protein precursor [H.sapiens]
4	AA091284	ESTs
2	AA092700	ESTs
1	AA092968	ESTs
4	AA094800	eukaryotic translation initiation factor 3; subunit 7 (zeta; 66/67kD)
4	AA100219	ESTs
4	AA114885	ESTs
4	AA129547	ESTs; Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]
4	AA133016	ESTs
3	AA149507	homolog of mouse quaking QKI (KH domain RNA binding protein)
2	AA151005	sperm surface protein
4	AA187101	zp61b6.r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:624659 5', mRNA sequence
3	AA195179_s	ESTs

Cluster	Accession # / PROBESET	Gene Description
2	AA203138	low density lipoprotein receptor (familial hypercholesterolemia)
2	AA203645	ESTs; Moderately similar to SH3-containing protein p415 [R.norvegicus]
3	AA206236	zq54c6.r1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:645418 5' similar to TR:G122922 G122922 ALLOGRAFT INFLAMMATORY FACTOR-1. :, mRNA sequence
1	AA227621	ESTs; Weakly similar to weak similarity to collagens [C.elegans]
4	AA248283	ESTs; Weakly similar to X-linked retinopathy protein {C-terminal; clone XEH.8c} [H.sapiens]
3	AA249611	H.sapiens mRNA for 21-Glutamic Acid-Rich Protein (21-GARP)
2	AA282640	ESTs
2	AA287199	Human mRNA for KIAA81 gene; partial cds
2	AA313990	ESTs; Highly similar to HYPOTHETICAL 3.5 KD PROTEIN C3A5.3 IN CHROMOSOME III [Caenorhabditis elegans]
2	AA314256	EST18611 Colon carcinoma (HCC) cell line II Homo sapiens cDNA 5' end, mRNA sequence
2	AA314389	ESTs; Highly similar to ADP-RIBOSYLATION FACTOR 1 [Saccharomyces cerevisiae]
2	AA324364	ESTs; Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]
3	AA329211_s	ESTs
2	AA399187	ESTs
4	AA421079	ESTs
2	AA422029	ESTs
3	AA425230	Human GAP SH3 binding protein mRNA; complete cds
4	AA447052	ESTs; Highly similar to N-terminal asparagine amidohydrolase [M.musculus]
4	AA452000	ESTs
4	AA456687	ESTs
4	AA487015_s	ESTs; Weakly similar to X-linked retinopathy protein {C-terminal; clone XEH.8c} [H.sapiens]
2	AB002326	Human mRNA for KIAA328 gene; partial cds
4	AFFX-BioB-3	.
2	C01527	ESTs
4	C01714	Homo sapiens serum-inducible kinase mRNA; complete cds
3	C01811_f	ESTs
2	C02352_s	ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]
1	C02375	Human mRNA containing an Alu repeat and its reverse complement
2	C14448	EST
4	D16611_s	coproporphyrinogen oxidase (coproporphyria; harderoporphyria)
2	D25216	Human mRNA for KIAA14 gene; complete cds
2	D31352	ESTs; Weakly similar to hypothetical protein [H.sapiens]

Cluster	Accession # PROBESET	Gene Description
4	D58024_s	ESTs; Weakly similar to probable hormone receptor EMR1 precursor [H.sapiens]
1	D80897	Homo sapiens clone 24736 mRNA sequence
3	D82614	ESTs
4	D87845	platelet-activating factor acetylhydrolase 2 (4kD)
1	D89377_i	msh (Drosophila) homeo box homolog 2
2	H06583	cAMP responsive element binding protein-like 2
1	H40732	ESTs
4	H46617	yp19h1.r1 Soares breast 3NbHBst Homo sapiens cDNA clone IMAGE:187921 5', mRNA sequence
1	H56731	ESTs
1	H75570	ESTs
2	H78886	ESTs
1	H81241	ESTs; Highly similar to ERYTHROID KRUEPPEL-LIKE TRANSCRIPTION FACTOR [Mus musculus]
1	L36531	integrin; alpha 8
2	M63154	gastric intrinsic factor (vitamin B synthesis)
4	M63180	threonyl-tRNA synthetase
2	M91504	ESTs
2	N56191	Homo sapiens protocadherin 68 (PCH68) mRNA; complete cds
2	N78483	ESTs
2	N79268	zinc finger protein 198
2	R14652	Homo sapiens PAC clone DJ872F7 from 7q31
2	R20459	yg33f12.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:34345 5', mRNA sequence
3	R22303	ESTs; Weakly similar to putative p15 [H.sapiens]
2	R33779	ESTs; Weakly similar to p4 [H.sapiens]
2	R36553	ESTs; Weakly similar to KIAA681 protein [H.sapiens]
2	R64534	ESTs
4	R66475	ESTs
4	R70621	Homo sapiens mRNA for KIAA896 protein; partial cds
3	R79356	ESTs; Weakly similar to PROTEIN Q3 [Mus musculus]
2	R84933	ESTs; Weakly similar to putative p15 [H.sapiens]
3	RC_AA007160	ESTs
2	RC_AA007234_s	ESTs; Highly similar to protein tyrosine phosphatase epsilon cytoplasmic isoform [H.sapiens]
2	RC_AA018409	ESTs
4	RC_AA025351	ESTs
3	RC_AA027168	ESTs
1	RC_AA027317	ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]
3	RC_AA029423	ESTs
4	RC_AA031357	ESTs
4	RC_AA045136	ESTs
1	RC_AA053400	ESTs

Cluster	Accession # / PROBESET	Gene Description
3	RC_AA055829	ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]
3	RC_AA065217	ESTs
1	RC_AA116054	ESTs
1	RC_AA126311	ESTs
4	RC_AA129390	ESTs
4	RC_AA130273	ESTs; Highly similar to DOSAGE COMPENSATION REGULATOR [Drosophila melanogaster]
2	RC_AA142919	ESTs
4	RC_AA150205	ubiquitous Kruppel-like transcription factor
1	RC_AA176867	ESTs
2	RC_AA180321	ESTs; Highly similar to U1 small nuclear ribonucleoprotein 1SNRP homolog [H.sapiens]
2	RC_AA180487	Homo sapiens TACC1 (TACC1) mRNA; complete cds
4	RC_AA187634	eukaryotic translation initiation factor 3; subunit 1 (alpha; 35kD)
3	RC_AA195399	ESTs
3	RC_AA234717	ESTs
4	RC_AA234743	ESTs
3	RC_AA234957	Homo sapiens mRNA for MTMR1 protein
3	RC_AA235604	ESTs
3	RC_AA236559	ESTs; Weakly similar to PROBABLE E5 PROTEIN [Human papillomavirus type 58]
3	RC_AA242868	ESTs; Weakly similar to house-keeping protein [M.musculus]
4	RC_AA251776	jun D proto-oncogene
4	RC_AA251909	Homo sapiens protein kinase homolog (BUBR1) mRNA; complete cds
3	RC_AA252672_s	diptheria toxin resistance protein required for diphthamide biosynthesis (Saccharomyces)-like 2
3	RC_AA256157	ESTs
4	RC_AA256680	ESTs
3	RC_AA258873	ESTs
1	RC_AA262727	ESTs
4	RC_AA281451	ESTs
4	RC_AA281545	ESTs
3	RC_AA282069	Homo sapiens mRNA for KIAA63 protein; complete cds
1	RC_AA283044	ESTs
3	RC_AA283930	ESTs
4	RC_AA284755	ESTs; Weakly similar to unknown [H.sapiens]
4	RC_AA291268	ESTs
1	RC_AA291927	ESTs
2	RC_AA343514	ESTs
3	RC_AA398109	ESTs
4	RC_AA405737	ESTs
4	RC_AA406610	ESTs
4	RC_AA411465	ESTs
3	RC_AA416886	ESTs; Weakly similar to predicted using Genefinder [C.elegans]

Cluster	Accession #/ PROBESET	Gene Description
4	RC_AA424013	Homo sapiens clone 23767 and 23782 mRNA sequences
4	RC_AA424148	ESTs
2	RC_AA424558	ESTs; Weakly similar to 33-kDa phototransducing protein [H.sapiens]
4	RC_AA424961_s	Homo sapiens TEB4 protein mRNA; complete cds
3	RC_AA425367	ESTs
1	RC_AA425921	Homo sapiens I-1 receptor candidate protein mRNA; complete cds
4	RC_AA426220	Homo sapiens mRNA for KIAA523 protein; partial cds
4	RC_AA427735	ESTs
4	RC_AA430673	ESTs
4	RC_AA432248	ESTs
4	RC_AA435896	ESTs
3	RC_AA436705	Homo sapiens mRNA for KIAA766 protein; complete cds
3	RC_AA446561	Homo sapiens mRNA for KIAA47 protein; complete cds
4	RC_AA448238	Homo sapiens mRNA for KIAA915 protein; complete cds
3	RC_AA448688	ESTs; Weakly similar to KIAA638 protein [H.sapiens]
3	RC_AA449756	ESTs; Weakly similar to rA8 [R.norvegicus]
4	RC_AA450303	ESTs
3	RC_AA452411	ESTs
4	RC_AA454566	ribosomal protein L13
4	RC_AA454667	ESTs
4	RC_AA456437	ESTs
4	RC_AA456646	ESTs
4	RC_AA456826	ESTs
4	RC_AA456981	ESTs
4	RC_AA458959	ESTs
3	RC_AA459950	ESTs
3	RC_AA460449	ESTs; Highly similar to PROBABLE PHOSPHOSERINE AMINOTRANSFERASE [Oryctolagus cuniculus]
3	RC_AA463910	ESTs
4	RC_AA464603	ESTs
3	RC_AA464606	ESTs
4	RC_AA465093	TIA1 cytotoxic granule-associated RNA-binding protein
3	RC_AA465692	Homo sapiens mRNA for KIAA648 protein; partial cds
3	RC_AA476473	Homo sapiens Trio mRNA; complete cds
1	RC_AA478109	ESTs
4	RC_AA478474	ESTs
3	RC_AA480889	ESTs
1	RC_AA485223	ESTs
1	RC_AA485254	ESTs
4	RC_AA486183	ESTs; Weakly similar to Yhr1wp [S.cerevisiae]
3	RC_AA496936	ESTs; Weakly similar to B cell growth factor [H.sapiens]
4	RC_AA598589	ESTs
4	RC_AA598831_f	ESTs
4	RC_AA600150	ESTs

Cluster	Accession # / PROBESET	Gene Description
4	RC_AA608545	ESTs
3	RC_AA609210	ESTs
3	RC_AA610108	ESTs; Highly similar to PROBABLE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE C21E11.5C [Schizosaccharomyces pombe]
4	RC_AA620582	ESTs; Weakly similar to (defline not available 424227) [H.sapiens]
4	RC_AA621239	ESTs; Highly similar to HYPOTHETICAL 98.3 KD PROTEIN R1E12.1 IN CHROMOSOME III [Caenorhabditis elegans]
3	RC_AA621714	ESTs
1	RC_AA621718	ESTs
1	RC_D19673	ESTs
1	RC_D25755_s	ESTs
1	RC_D51095	ESTs
4	RC_D60272_i	ESTs; Weakly similar to macrophage lectin 2 [H.sapiens]
2	T08879	cathepsin F
3	T34527	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1)
2	T40327_s	ESTs
3	T62771_s	Homo sapiens nucleoplasmin-3 (NPM3) mRNA; complete cds
1	T63174_s	ESTs; Weakly similar to neuronal thread protein AD7c-NTP [H.sapiens]
2	T83444	Homo sapiens mRNA for KIAA887 protein; partial cds
1	T93641	ESTs
2	U48263	prepronociceptin
2	U49065	interleukin 1 receptor-like 2
2	U79300	Human clone 23629 mRNA sequence
1	U88573	Human NBR2 mRNA; complete cds
2	U93867	Human RNA polymerase III subunit (RPC62) mRNA; complete cds
4	W01094	ESTs
2	W01568	ESTs
2	W26853	ESTs
2	W27179	BCL2/adenovirus E1B 19kD-interacting protein 3-like
2	W27965	epimorphin
3	W36280_s	Homo sapiens RRM RNA binding protein Gry-rbp (GRY-RBP) mRNA; complete cds
2	W47063	ESTs
4	W79060	ESTs; Weakly similar to Ras-binding protein SUR-8 [M.musculus]
4	W88550	ESTs; Moderately similar to trg gene product [R.norvegicus]
1	X60486	H4 histone family; member G
2	X78931_s	H.sapiens HZF8 mRNA for zinc finger protein
1	Z14077_s	YY1 transcription factor
1	RC_AA002147	EST
1	RC_AA004711	ESTs
1	RC_AA010383	EST
1	RC_AA015761	ESTs

Cluster	Accession # / PROBESET	Gene Description
2	RC_AA018772	ESTs
2	RC_AA021473_r	EST
2	RC_AA024835	potassium voltage-gated channel; delayed-rectifier; subfamily S; member 3
2	RC_AA025858	ESTs
1	RC_AA027229	ESTs
1	RC_AA029428	ESTs
3	RC_AA035143	ESTs
1	RC_AA035237	ESTs
2	RC_AA039347	EST
1	RC_AA040740	ESTs
3	RC_AA041551	ESTs
1	RC_AA045513	ESTs
1	RC_AA045745	EST
1	RC_AA055348	ESTs
2	RC_AA056582_s	ESTs
1	RC_AA056697	ESTs
1	RC_AA056746	EST
3	RC_AA057678	ESTs
2	RC_AA058681	ESTs
2	RC_AA058686	ESTs
2	RC_AA062840	zm5c1.s1 Stratagene corneal stroma (#937222) Homo sapiens cDNA clone IMAGE:513234 3' similar to gb:S71381 PROTEASOME BETA CHAIN (HUMAN);, mRNA sequence
2	RC_AA064859	zm5f3.s1 Stratagene fibroblast (#937212) Homo sapiens cDNA clone IMAGE:52985 3', mRNA sequence
1	RC_AA065069	zm12e11.s1 Stratagene pancreas (#93728) Homo sapiens cDNA clone IMAGE:525452 3', mRNA sequence
1	RC_AA069923	zm67g3.s1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:5374 3' similar to gb:S66915_cds1 ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR (HUMAN);, mRNA sequence
2	RC_AA070799_s	zm6h5.s1 Stratagene fibroblast (#937212) Homo sapiens cDNA clone IMAGE:5373 3', mRNA sequence
2	RC_AA070815	zm6a1.s1 Stratagene fibroblast (#937212) Homo sapiens cDNA clone IMAGE:529992 3' similar to gb:X67951 PROLIFERATION-ASSOCIATED PROTEIN PAG (HUMAN);, mRNA sequence
2	RC_AA075374	zm87a1.s1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:544872 3', mRNA sequence
2	RC_AA076382	zm91g8.s1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:545342 3', mRNA sequence
1	RC_AA078787	ESTs

Cluster	Accession # / PROBESET	Gene Description
2	RC_AA078986	zm92h1.s1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:545425 3', mRNA sequence
1	RC_AA079393	zm95h11.s1 Stratagene colon HT29 (#937221) Homo sapiens cDNA clone IMAGE:545733 3' similar to gb:X1656 CYTOCHROME C OXIDASE POLYPEPTIDE VIIC PRECURSOR (HUMAN);, mRNA sequence
2	RC_AA079487	zm97f8.s1 Stratagene colon HT29 (#937221) Homo sapiens cDNA clone IMAGE:545895 3', mRNA sequence
2	RC_AA083207	EST
2	RC_AA083256	vinculin
2	RC_AA084415	zn6g9.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:546688 3', mRNA sequence
2	RC_AA085274	zn1f1.s1 Stratagene colon HT29 (#937221) Homo sapiens cDNA clone IMAGE:546169 3' similar to gb:X15341 CYTOCHROME C OXIDASE POLYPEPTIDE VIA-LIVER (HUMAN);, mRNA sequence
2	RC_AA088678	ESTs
3	RC_AA100925	ESTs; Weakly similar to predicted using Genefinder [C.elegans]
3	RC_AA101255	ESTs; Highly similar to J KAPPA-RECOMBINATION SIGNAL BINDING PROTEIN [Homo sapiens]
3	RC_AA126474	stanniocalcin 2
2	RC_AA127017	ESTs
2	RC_AA129968	ESTs; Weakly similar to protein phosphatase 2A 13 kDa regulatory subunit [H.sapiens]
2	RC_AA130240	ESTs
1	RC_AA131866	ESTs
2	RC_AA132039	ESTs; Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]
3	RC_AA132983	ESTs; Moderately similar to C-1-TETRAHYDROFOLATE SYNTHASE; CYTOPLASMIC [Saccharomyces cerevisiae]
3	RC_AA133250	ESTs; Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 [Caenorhabditis elegans]
1	RC_AA133583_s	high-mobility group (nonhistone chromosomal) protein isoform I-C
4	RC_AA135941	ESTs
2	RC_AA148650	zo9e6.s1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:56722 3', mRNA sequence
2	RC_AA151110	ESTs
2	RC_AA155754	ESTs; Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]
4	RC_AA156125	ESTs
2	RC_AA156289	ESTs
1	RC_AA156997	ESTs
2	RC_AA157291	ESTs

Cluster	Accession #/ PROBESET	Gene Description
2	RC_AA157293	ESTs
2	RC_AA164293_f	ESTs
1	RC_AA164676	EST
1	RC_AA167375	Homo sapiens mRNA for KIAA53 protein; partial cds
1	RC_AA167550	ESTs; Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]
2	RC_AA176589	EST
1	RC_AA180448	EST
4	RC_AA187144_s	endothelin 1
3	RC_AA189170_f	ESTs
4	RC_AA192757	ESTs
2	RC_AA205650	ESTs
4	RC_AA233342	ESTs; Weakly similar to neural differentiation-associated protein [M.musculus]
3	RC_AA233472	ESTs
2	RC_AA234110	ESTs
4	RC_D80981	ESTs
3	RC_F01660	ESTs; Weakly similar to HYPOTHETICAL PROTEIN HI34 [Haemophilus influenzae]
1	RC_F02206	EST; Highly similar to ether-a-go-go-related protein [H.sapiens]
4	RC_F02208	ESTs
4	RC_F02544	ESTs
4	RC_F03918	ESTs
4	RC_F04258_s	ESTs; Highly similar to INORGANIC PYROPHOSPHATASE [Bos taurus]
4	RC_F04600	ESTs
4	RC_F08998	ESTs
2	RC_F09605	ESTs
4	RC_F11115	ESTs
3	RC_H06371	ESTs
1	RC_H10995	ESTs
1	RC_H11938	ESTs; Weakly similar to HYPOTHETICAL 97.6 KD PROTEIN IN SHP1-SEC17 INTERGENIC REGION [Saccharomyces cerevisiae]
4	RC_H16568	ESTs
4	RC_H16772	ESTs
1	RC_H18951	ESTs; Moderately similar to seven-pass transmembrane receptor precursor [M.musculus]
1	RC_H20859	ESTs
1	RC_H23747	ESTs
1	RC_H38087	ESTs
1	RC_H40331	ESTs
1	RC_H40567	ESTs

Cluster	Accession # PROBESET	Gene Description
1	RC_H46966	ESTs
1	RC_H56640_i	yq99a5.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:23888 3', mRNA sequence
1	RC_H57154	ESTs; Weakly similar to RST [M.musculus]
1	RC_H96712	ESTs
1	RC_N20814	ESTs
3	RC_N25249	synaptosomal-associated protein; 23kD
1	RC_N27100	ESTs
1	RC_N39616	RNA (guanine-7-) methyltransferase
1	RC_N48982	ESTs
1	RC_N51957	ESTs
1	RC_N52271	Homo sapiens LIM protein mRNA; complete cds
1	RC_N59435	ESTs; Weakly similar to No definition line found [H.sapiens]
1	RC_N64139	ESTs; Weakly similar to Ndr protein kinase [H.sapiens]
3	RC_N66981	ESTs
1	RC_N68640	ESTs
4	RC_N69352	ESTs; Highly similar to PRE-MRNA SPLICING FACTOR RNA HELICASE PRP22 [Saccharomyces cerevisiae]
4	RC_N95226	Homo sapiens mRNA for KIAA758 protein; partial cds
1	RC_R00138	ESTs
1	RC_R07998	ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]
1	RC_R08929	ubiquitin-conjugating enzyme E2G 2 (homologous to yeast UBC7)
1	RC_R10307	ESTs
3	RC_R33354	ESTs
1	RC_R36083	ESTs
1	RC_R37938_f	ESTs
1	RC_R39330	yd1g4.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:24282 3', mRNA sequence
1	RC_R40816_s	cullin 4A
1	RC_R43162_s	ESTs
3	RC_R45698	ESTs; Weakly similar to Similarity to Salmonella regulatory protein UHPC [C.elegans]
2	RC_R54554	ESTs
1	RC_R68425	ESTs; Weakly similar to alternatively spliced product using exon 13A [H.sapiens]
1	RC_R68568	ESTs
3	RC_R68763	ESTs
1	RC_R70467	ESTs
1	RC_R73565	ESTs; Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]
4	RC_R73640	ESTs

Cluster	Accession #/ PROBESET	Gene Description
1	RC_R78376	EST
1	RC_R92453	EST
1	RC_T03865	ESTs
3	RC_T03872	ESTs
1	RC_T10072	ESTs
1	RC_T10080	ESTs
1	RC_T10132	Homo sapiens mRNA for KIAA478 protein; complete cds
1	RC_T15343	ESTs
2	RC_T23457	ESTs
1	RC_T23555	ESTs
2	RC_T23670	ESTs
4	RC_T23948	ESTs
4	RC_T33464	ESTs
1	RC_T34413	ESTs
2	RC_T34611	ESTs
2	RC_T40920	ESTs
4	RC_T55182	ESTs
2	RC_T77453	EST
1	RC_T84039	ESTs
1	RC_T86458	ESTs
1	RC_T87693	ESTs
2	RC_T89350_s	ESTs
1	RC_T90945	ESTs
2	RC_T90987	ESTs
1	RC_T91863	ESTs
1	RC_T91881	EST
1	RC_T93783_s	ESTs
1	RC_T96687	ESTs
2	RC_T96944	ESTs
3	RC_T97307	ESTs; Weakly similar to neuronal thread protein AD7c-NTP [H.sapiens]
1	RC_T97764	ESTs
2	RC_W48817	ESTs
2	RC_W58343	ESTs
1	RC_W59949	ESTs; Highly similar to RAS-LIKE PROTEIN TC1 [Homo sapiens]
1	RC_W74644	ESTs
1	RC_W74761	ESTs; Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD [Caenorhabditis elegans]
1	RC_W74802	ESTs
1	RC_W81205	ESTs
2	RC_W81237	ESTs
3	RC_W90146_f	ESTs
1	RC_W92798	ESTs
1	RC_Z38412	EST
1	RC_Z38709	inositol 1;4;5-triphosphate receptor; type 2

Cluster	Accession # / PROBESET	Gene Description
1	RC_Z38904	ESTs
2	RC_Z39103	core-binding factor; runt domain; alpha subunit 2; translocated to; 2
2	RC_Z39930_f	ESTs
2	RC_Z39939	ESTs
3	RC_Z40012_i	Homo sapiens mRNA for KIAA587 protein; complete cds
2	RC_Z40377_s	ESTs
1	RC_Z40820	ESTs
3	RC_Z41680	ESTs
4	AFFX-BioB-3	.
2	RC_AA005112	Human zinc-finger domain-containing protein mRNA; partial cds
4	RC_AA005432	ESTs; Highly similar to ANTI-SILENCING PROTEIN 1 [Saccharomyces cerevisiae]
4	RC_AA010163	Human mRNA for KIAA312 gene; partial cds
4	RC_AA026356	ESTs
2	RC_AA026901	ESTs
4	RC_AA036867	ESTs
1	RC_AA044644	Pp52
4	RC_AA046426	Homo sapiens MSE55-related protein (UB1) mRNA; complete cds
4	RC_AA054515	ESTs; Weakly similar to X-linked retinopathy protein {C-terminal; clone XEH.8c} [H.sapiens]
2	RC_AA084162	zn17h6.s1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:547739 3', mRNA sequence
4	RC_AA085749	Homo sapiens mRNA for ATP binding protein; complete cds
4	RC_AA098874	ESTs
2	RC_AA101056	zn25b3.s1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548429 3' similar to contains L1.b3 L1 repetitive element ;, mRNA sequence
1	RC_AA102746	ESTs; Moderately similar to cytotoxic ligand TRAIL receptor [H.sapiens]
2	RC_AA114250_s	Homo sapiens mRNA for KIAA512 protein; complete cds
4	RC_AA126561_s	ESTs
4	RC_AA128980_i	ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]
4	RC_AA129757	ESTs; Highly similar to 6S RIBOSOMAL PROTEIN L22 [Rattus norvegicus]
4	RC_AA129921	ESTs
2	RC_AA133331	Homo sapiens mRNA for KIAA741 protein; complete cds
2	RC_AA135958	ESTs
4	RC_AA136524_s	ESTs
4	RC_AA147044	ESTs; Weakly similar to transformation-related protein [H.sapiens]
4	RC_AA148885	ESTs
4	RC_AA150043	ESTs
2	RC_AA151621	ESTs
4	RC_AA155743	ESTs

Cluster	Accession # / PROBESET	Gene Description
2	RC_AA156335	ESTs
4	RC_AA156336	Homo sapiens nuclear receptor co-repressor N-CoR mRNA; complete cds
2	RC_AA159181	ESTs
2	RC_AA159825	ESTs
2	RC_AA234185	ESTs
4	RC_AA234929	ESTs
1	RC_AA234935	ESTs
4	RC_AA236359	ESTs
2	RC_AA236466	ESTs
2	RC_AA236535	ESTs
4	RC_AA236935_s	Human normal keratinocyte mRNA
2	RC_AA236942	ESTs
4	RC_AA237018	ESTs
2	RC_AA237025	ESTs
2	RC_AA242751	Homo sapiens mRNA for KIAA93 protein; partial cds
3	RC_AA242760	ESTs
3	RC_AA242763	Homo sapiens Cdc14B1 phosphatase mRNA; complete cds
2	RC_AA242809	ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]
3	RC_AA243133	ESTs; Highly similar to SERINE/THREONINE-PROTEIN KINASE IPL1 [Saccharomyces cerevisiae]
4	RC_AA243495	ESTs
3	RC_AA243706	ESTs
4	RC_AA250848	zs6e2.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:68441 3', mRNA sequence
2	RC_AA250868	ESTs
4	RC_AA251152	ESTs
2	RC_AA251544_s	ESTs
4	RC_AA251792	ESTs
4	RC_AA252063	Homo sapiens mRNA for PCDH7 (BH-Pcdh)c; complete cds
3	RC_AA252144	ESTs
4	RC_AA252524	ESTs
3	RC_AA253461	ESTs
4	RC_AA255522	ESTs
2	RC_AA256468	ESTs
4	RC_AA256528	ESTs
2	RC_AA257976	ESTs
4	RC_AA258296	Homo sapiens mRNA for KIAA579 protein; partial cds
3	RC_AA258409	H.sapiens gene from PAC 313L4; similar to Myelin PO
2	RC_AA258421	Homo sapiens clone 683 unknown mRNA; complete sequence

Cluster	Accession # PROBESET	Gene Description
3	RC_AA262077	Human NAD+-dependent succinate-semialdehyde dehydrogenase (SSADH) mRNA; 3' end
4	RC_AA278650	ESTs
2	RC_AA278766	ESTs
4	RC_AA279667_s	natural killer-tumor recognition sequence
3	RC_AA280791	eukaryotic translation initiation factor 5
4	RC_AA280819	ESTs
4	RC_AA280828	ESTs
4	RC_AA282195	ESTs; Weakly similar to ORF YNL292w [S.cerevisiae]
2	RC_AA283127_s	Homo sapiens clone LM1955 H15e3 gene; partial cds
2	RC_AA284694	Homo sapiens CG1 mRNA; complete cds
3	RC_AA291137	ESTs
3	RC_AA291708	ESTs; Moderately similar to hypothetical protein [H.sapiens]
3	RC_AA293495	Homo sapiens BAC clone 255A7 from 8q21 containing NBS1 gene; complete sequence
4	RC_AA347193	ESTs; Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 [Caenorhabditis elegans]
4	RC_AA398474_s	ESTs
4	RC_AA398512	ESTs
2	RC_AA400277	ESTs; Weakly similar to putative p15 [H.sapiens]
4	RC_AA400896	ESTs
3	RC_AA404494	CTP synthase
2	RC_AA410345	ESTs; Weakly similar to A33 antigen precursor [H.sapiens]
4	RC_AA416733	ESTs; Weakly similar to neuronal thread protein AD7c-NTP [H.sapiens]
4	RC_AA425154	ESTs
4	RC_AA426573	ESTs
2	RC_AA431418	N-acetylglucosaminidase; alpha- (Sanfilippo disease IIIB)
4	RC_AA436182	ESTs
2	RC_AA437099	ESTs
4	RC_AA446585	ESTs
3	RC_AA446887	ESTs
2	RC_AA447224	ESTs; Highly similar to HYPOTHETICAL 8.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION [Saccharomyces cerevisiae]
2	RC_AA447709	ESTs; Moderately similar to putative transcription factor CA15 [H.sapiens]
4	RC_AA453624	deoxynucleotidyltransferase; terminal
4	RC_AA455044	ESTs
4	RC_AA456045	ESTs
4	RC_AA460454_s	ESTs; Weakly similar to KIAA512 protein [H.sapiens]
4	RC_AA476494	ESTs; Weakly similar to KIAA512 protein [H.sapiens]
4	RC_AA476738	ESTs; Highly similar to FLI-LRR associated protein-1 [M.musculus]
4	RC_AA481422	Homo sapiens mRNA for H-2K binding factor-2; complete cds
3	RC_AA482269	integral membrane protein 1

Cluster	Accession # / PROBESET	Gene Description
2	RC_AA482595	ESTs; Highly similar to p36
4	RC_AA485084_s	ESTs
4	RC_AA485431_s	ESTs
4	RC_AA489057	H.sapiens mRNA for nuclear protein SA-2
4	RC_AA489638	ESTs
2	RC_AA491000	ESTs
3	RC_AA491250	ESTs
4	RC_AA505133	ESTs
4	RC_AA598447	Homo sapiens exportin t mRNA; complete cds
3	RC_AA599243	ESTs
3	RC_AA599574_l	ESTs
4	RC_AA600153	DEK gene
4	RC_AA609309	ESTs
4	RC_AA609710	ESTs; Highly similar to HYPOTHETICAL GTP-BINDING PROTEIN IN PMI4-PAC2 INTERGENIC REGION [Saccharomyces cerevisiae]
4	RC_AA610068	H.sapiens mRNA for PIBF1 protein; complete
1	RC_AA621399	ESTs
4	RC_AA621752	Human 26S proteasome-associated pad1 homolog (POH1) mRNA; complete cds
2	RC_C21523	ESTs
2	RC_D12160	ESTs; Weakly similar to unknown [H.sapiens]
4	RC_D19708	ESTs
2	RC_D25801	ESTs; Highly similar to KIAA445 protein [H.sapiens]
2	RC_D45652	ESTs; Weakly similar to unknown [H.sapiens]
4	RC_D60208_f	ESTs
3	RC_D80504_s	zinc finger protein 198
2	RC_F03010	ESTs; Weakly similar to ZINC FINGER PROTEIN HRX [Homo sapiens]
4	RC_F04247	ESTs; Weakly similar to !!!! ALU CLASS A WARNING ENTRY !!!! [H.sapiens]
4	RC_F10966	ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]
4	RC_F13700	Homo sapiens ribonuclease P protein subunit p4 (RPP4) gene; complete cds
4	RC_H05063	ESTs
4	RC_H16758	ESTs; Highly similar to ERYTHROPOIETIN RECEPTOR PRECURSOR [Homo sapiens]
4	RC_H17315_s	karyopherin alpha 1 (importin alpha 5)
4	RC_H22556	PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG
4	RC_H22566	ESTs; Highly similar to protein tyrosine phosphatase epsilon cytoplasmic isoform [H.sapiens]
4	RC_H48459_s	Human mRNA for KIAA186 gene; complete cds
4	RC_H53073	ESTs
2	RC_H56559_s	Homo sapiens mRNA for KIAA61 protein; partial cds
3	RC_H57957_s	ESTs

Cluster	Accession #/ PROBESET	Gene Description
2	RC_H64938_s	ESTs
2	RC_H64973	ESTs
4	RC_H69535	ESTs
2	RC_H73110	ESTs; Moderately similar to alternatively spliced product using exon 13A [H.sapiens]
2	RC_H81783	ESTs
1	RC_H86259	Homo sapiens chromosome 19; cosmid R32611
2	RC_H88353	ESTs; Weakly similar to reverse transcriptase related protein [H.sapiens]
2	RC_H88639	ESTs
4	RC_H88675	ESTs
4	RC_H93708_s	CLEAVAGE SIGNAL-1 PROTEIN
4	RC_N22107	ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]
3	RC_N24046	ESTs; Weakly similar to 6S RIBOSOMAL PROTEIN L1 [Homo sapiens]
2	RC_N27028	ESTs
2	RC_N30205	ESTs; Weakly similar to hypothetical protein [H.sapiens]
1	RC_N30621	ESTs
4	RC_N33258	Homo sapiens nuclear receptor co-repressor N-CoR mRNA; complete cds
2	RC_N33390	EST
2	RC_N40180	EST; Weakly similar to putative p15 [H.sapiens]
2	RC_N45198	EST
3	RC_N45979_s	SH3 domain protein 1B
2	RC_N48325	EST
2	RC_N48913	ESTs
4	RC_N49394	Homo sapiens mRNA for KIAA716 protein; complete cds
1	RC_N50656	ESTs; Highly similar to mosaic protein LR11 [H.sapiens]
4	RC_N50721	kinesin family protein 3B
4	RC_N53143	ESTs
2	RC_N53359	ESTs
4	RC_N55326	ESTs
2	RC_N55493	yv5c2.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:246146 3', mRNA sequence
4	RC_N57493	EST
2	RC_N62955	ESTs; Weakly similar to ankyrin G [H.sapiens]
4	RC_N63520	EST; Weakly similar to mariner transposase [H.sapiens]
4	RC_N63604	ESTs
2	RC_N64166	frizzled (Drosophila) homolog 7
2	RC_N64168	ESTs
2	RC_N64191	ESTs
4	RC_N66845	ESTs; Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]
4	RC_N67135	ESTs

Cluster	Accession # / PROBESET	Gene Description
2	RC_N67295	ESTs
4	RC_N68399	H2B histone family; member N
4	RC_N68963	ESTs
4	RC_N69331	peptidylprolyl isomerase C (cyclophilin C)
2	RC_N70777	ESTs
1	RC_N71364_s	ESTs; Weakly similar to transformation-related protein [H.sapiens]
4	RC_N71545_s	ESTs; Moderately similar to hypothetical protein [H.sapiens]
2	RC_N71571	ESTs
4	RC_N74456	EST
4	RC_N75594	ESTs
2	RC_N79035	EST
2	RC_N80279	ESTs; Highly similar to (defline not available 4239677) [H.sapiens]
4	RC_N91797	ESTs
4	RC_N92454	karyopherin (importin) beta 1
4	RC_N94581	actin; beta
4	RC_N94746	ESTs
4	RC_N98238	ESTs
4	RC_R02384	EST
2	RC_R16833	ESTs; Weakly similar to !!!! ALU CLASS F WARNING ENTRY !!!! [H.sapiens]
3	RC_R41828_s	myosin VA (heavy polypeptide 12; myoxin)
2	RC_R43203	ESTs
4	RC_R46395	ESTs; Moderately similar to Unknown gene product [H.sapiens]
2	RC_R58863	ESTs
2	RC_R78248	ESTs
4	RC_T11483	ESTs
4	RC_T16896	ESTs
2	RC_T23820	cyclin T2
4	RC_T30222	ESTs; Weakly similar to tetracycline transporter-like protein [M.musculus]
4	RC_W15275_s	ESTs
2	RC_W38194	Accession not listed in Genbank
3	RC_W42414_s	ESTs
4	RC_W46577_s	H.sapiens mRNA for ESM-1 protein
4	RC_W49632_s	Human clone 2398 mRNA sequence
2	RC_W57613.	ESTs
2	RC_W57759	EST
4	RC_W61118	ESTs
4	RC_W65344	ESTs; Highly similar to ICH-2 PROTEASE PRECURSOR [Homo sapiens]
2	RC_W69216	ESTs
2	RC_W69379	ESTs; Weakly similar to mitochondrial inner membrane protease 1 [S.cerevisiae]
4	RC_W86728	ESTs

Cluster	Accession # / PROBESET	Gene Description
4	RC_Z38499	ESTs; Weakly similar to protein phosphatase [H.sapiens]
2	RC_Z38630	Homo sapiens 1kD protein (BC1) mRNA; complete cds
4	RC_Z39494	ESTs
4	RC_Z39623	ESTs
3	RC_Z40071_s	BMX non-receptor tyrosine kinase
2	RC_Z40174	EST
2	RC_Z40182	EST
2	RC_Z40904	EST
4	AFFX-BioB-3	.
4	AFFX-BioC-3	.
3	AFFX-DapX-5	.
1	AFFX-LysX-M	.
3	RC_AA166965	ESTs
3	RC_AA167500	EST
1	RC_AA169599_s	ESTs
3	RC_AA171724	ESTs
2	RC_AA171739	ESTs
3	RC_AA177105	ESTs
2	RC_AA182626	ESTs
3	RC_AA186324	ESTs; Highly similar to cell cycle progression restoration 8 protein [H.sapiens]
1	RC_AA192099	zinc finger protein 148 (pHZ-52)
3	RC_AA192173	ESTs; Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]
3	RC_AA192415	EST
3	RC_AA192553	ESTs; Moderately similar to RGC-32 [R.norvegicus]
3	RC_AA194851	ESTs
3	RC_AA195520_s	ESTs
3	RC_AA196300	ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]
3	RC_AA196517	Lon protease-like protein
3	RC_AA196549	ESTs
3	RC_AA196721	zq9a3.s1 Stratagene muscle 93729 Homo sapiens cDNA clone IMAGE:629164 3' similar to TR:G746415 G746415 I KAPPA BR. ;, mRNA sequence
3	RC_AA196729_i	ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]
1	RC_AA196979	ESTs; Moderately similar to RETROVIRUS-RELATED PROTEASE [H.sapiens]
2	RC_AA206828	ESTs; Weakly similar to ubiquitous TPR motif; Y isoform [H.sapiens]
3	RC_AA207123	immunoglobulin superfamily; member 3
1	RC_AA214539_i	ESTs
3	RC_AA226914_s	TR2 nuclear hormone receptor

Cluster	Accession # / PROBESET	Gene Description
3	RC_AA227260	Zic family member 3 (odd-paired Drosophila homolog; heterotaxy 1)
3	RC_AA227469	EST
3	RC_AA233122	ESTs; Highly similar to CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II DELTA CHAIN [Rattus norvegicus]
3	RC_AA233334_s	Homo sapiens josephin MJD1 mRNA; cds
3	RC_AA233347	Homo sapiens zinc finger protein 216 splice variant 2 (ZNF216) mRNA; complete cds
1	RC_AA233519	ESTs; Weakly similar to neuronal thread protein AD7c-NTP [H.sapiens]
1	RC_AA233714	Apg12 (autophagy; yeast) homolog
1	RC_AA233798	ESTs
1	RC_AA235050_f	ESTs
1	RC_AA235704	ESTs; Weakly similar to Wiscott-Aldrich Syndrome protein homolog [M.musculus]
3	RC_AA236031	ESTs
1	RC_AA236352	ESTs
1	RC_AA236390_s	ESTs
1	RC_AA236453	ESTs
3	RC_AA243370	EST
2	RC_AA250947	ESTs
3	RC_AA251083	ESTs
3	RC_AA251113	ESTs
4	RC_AA251973	ESTs
3	RC_AA252023	ESTs; Moderately similar to (defline not available 397874) [H.sapiens]
1	RC_AA252414	ESTs
1	RC_AA252650	protein kinase; mitogen-activated; kinase 7 (MAP kinase kinase 7)
3	RC_AA255523	ESTs
3	RC_AA258128	ESTs
3	RC_AA262105	Human mRNA for KIAA331 gene; complete cds
1	RC_AA262107	ESTs
1	RC_AA262235	ESTs
3	RC_AA278298	zs8b3.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:73757 3', mRNA sequence
1	RC_AA278529_i	ESTs; Highly similar to serine/threonine protein kinase [H.sapiens]
1	RC_AA278721	ESTs
1	RC_AA280036	ESTs
1	RC_AA280648	ESTs; Weakly similar to rab-related GTP-binding protein [H.sapiens]
1	RC_AA280738	ESTs
3	RC_AA280794	ESTs
1	RC_AA280837	ESTs
1	RC_AA280886	ESTs; Moderately similar to alternatively spliced product using exon 13A [H.sapiens]
1	RC_AA280934	ESTs
1	RC_AA281535	Homo sapiens mRNA for KIAA879 protein; complete cds

Cluster	Accession # / PROBESET	Gene Description
4	RC_AA281797_s	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene; partial cds; neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes; complete cds
1	RC_AA282047	ESTs
1	RC_AA283002	Human zinc finger protein (SRE-ZBP) mRNA; 3' end
3	RC_AA283709	ESTs
1	RC_AA283902	ESTs; Weakly similar to X-linked retinopathy protein {C-terminal; clone XEH.8c} [H.sapiens]
1	RC_AA284108	Human DNA from chromosome 19-specific cosmid F25965; genomic sequence
1	RC_AA284109	Human DNA sequence from clone 71L16 on chromosome Xp11. Contains a probable Zinc Finger protein (pseudo)gene; an unknown putative gene; a pseudogene with high similarity to part of antigen KI-67; a pu
1	RC_AA284371	Homo sapiens clone 23967 unknown mRNA; partial cds
3	RC_AA284744_f	ESTs
1	RC_AA284784	ESTs
1	RC_AA284840	ESTs
1	RC_AA286844	ESTs
3	RC_AA287032	ESTs
1	RC_AA287038	EST
1	RC_AA287546	ESTs
1	RC_AA287553_s	ESTs
3	RC_AA287556	ESTs; Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]
1	RC_AA287564	ribosomal protein L37
1	RC_AA291015_s	CDC7 (cell division cycle 7; S. cerevisiae; homolog)-like 1
3	RC_AA291716	EST
1	RC_AA291749_s	ESTs
1	RC_AA293656	EST
1	RC_AA302430	ESTs
3	RC_AA302809	EST
1	RC_AA302820_s	purinergic receptor P2X; ligand-gated ion channel; 4
1	RC_AA310499	ESTs
1	RC_AA321890	EST24442 Cerebellum II Homo sapiens cDNA 3' end, mRNA sequence
1	RC_AA340589	EST
1	RC_AA340622	ESTs
1	RC_AA342457_i	ESTs
3	RC_AA342828_s	glycoprotein V (platelet)
1	RC_AA342864	ESTs
1	RC_AA342973	ESTs
1	RC_AA346495	ESTs
1	RC_AA347573	Homo sapiens KIAA45 mRNA; complete cds
1	RC_AA347614	ESTs
1	RC_AA347717	ESTs

Cluster	Accession # / PROBESET	Gene Description
1	RC_AA348913	ESTs
1	RC_AA349647	EST
1	RC_AA349773	ESTs
1	RC_AA350541_s	ESTs; Moderately similar to alternatively spliced product using exon 13A [H.sapiens]
1	RC_AA357159_i	EST
3	RC_AA357172_i	ESTs
1	RC_AA369856_s	Human hVps41p (hVPS41) mRNA; alternative splice variant; partial cds
1	RC_AA370132	EST
1	RC_AA370472_s	ESTs
1	RC_AA370867	ESTs
3	RC_AA377296	ESTs
4	RC_AA383902	ESTs
3	RC_AA385934	EST; Highly similar to predicted using Genefinder [C.elegans]
3	RC_AA386255	EST
1	RC_AA386260	EST
2	RC_AA386266	ESTs; Highly similar to MEMBRANE GLYCOPROTEIN M6-B [Mus musculus]
1	RC_AA398014	ESTs
3	RC_AA398222	ESTs
1	RC_AA398235	ESTs
3	RC_AA398348	ESTs
3	RC_AA398482	ESTs
1	RC_AA398504	ESTs
1	RC_AA398505	ESTs
1	RC_AA398507	ESTs
1	RC_AA398523	ESTs; Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]
1	RC_AA398625	ESTs
4	RC_AA398632	ESTs
3	RC_AA398633	ESTs
3	RC_AA398894	ESTs
3	RC_AA398895	EST
1	RC_AA398900	ESTs
1	RC_AA398904	EST
1	RC_AA399122	ESTs; Weakly similar to mitochondrial citrate transport protein [H.sapiens]
3	RC_AA399371	ESTs
1	RC_AA399373	ESTs; Highly similar to KIAA568 protein [H.sapiens]
1	RC_AA399441	ESTs
3	RC_AA399636	ESTs
1	RC_AA399640	ESTs
1	RC_AA399680	ESTs

Cluster	Accession #/ PROBESET	Gene Description
3	RC_AA400080	EST
1	RC_AA400262	ESTs
1	RC_AA400725	ESTs
3	RC_AA400748	ESTs
1	RC_AA400780	ESTs
3	RC_AA401631	zv65b9.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:758489 3', mRNA sequence
1	RC_AA401688	ESTs
1	RC_AA401695	EST
3	RC_AA402227	ESTs; Moderately similar to N-tropomodulin [R.norvegicus]
3	RC_AA402329	ESTs
1	RC_AA402398	ESTs
1	RC_AA402449	EST
1	RC_AA402468	ESTs
2	RC_AA403268_s	ESTs
2	RC_AA403314	ESTs
1	RC_AA404229	EST
1	RC_AA404260	ESTs
1	RC_AA404271	Human glutamate/kainate receptor subunit (EEA3) mRNA; complete cds
3	RC_AA405026	ESTs
1	RC_AA405182	ESTs
1	RC_AA405237	ESTs; Moderately similar to alternatively spliced product using exon 13A [H.sapiens]
3	RC_AA406061	EST
1	RC_AA406063	ESTs
1	RC_AA406070	EST
1	RC_AA406137	EST
1	RC_AA406335	ESTs
1	RC_AA411801	Human mRNA for KIAA37 gene; complete cds
1	RC_AA411804	ESTs
1	RC_AA411833	ESTs; Highly similar to (defline not available 4521278) [H.sapiens]
1	RC_AA412219	ESTs
3	RC_AA412259	ESTs
2	RC_AA412497	Human Line-1 repeat mRNA with 2 open reading frames
1	RC_AA412498	ESTs
1	RC_AA416586	ESTs
1	RC_AA416867	EST
1	RC_AA416874	ESTs
1	RC_AA421133	ESTs
1	RC_AA421138	EST
4	RC_AA422079	ESTs; Highly similar to ELONGATION FACTOR G; MITOCHONDRIAL PRECURSOR [Rattus norvegicus]
1	RC_AA423837	ESTs
1	RC_AA424328	ESTs
1	RC_AA424339	ESTs

Cluster	Accession # / PROBESET	Gene Description
3	RC_AA424469_s	ESTs
1	RC_AA424502	ESTs
3	RC_AA425004	ESTs
1	RC_AA425734	ESTs; Weakly similar to neuronal thread protein AD7c-NTP [H.sapiens]
1	RC_AA425887	ESTs
3	RC_AA426456	ESTs
3	RC_AA427396	ESTs
1	RC_AA427555	Human mRNA for KIAA23 gene; complete cds
3	RC_AA428218	ESTs
3	RC_AA428242	ESTs
1	RC_AA428281	EST
3	RC_AA428865	EST
3	RC_AA428994	ESTs
1	RC_AA429666	ESTs
3	RC_AA430181	ESTs
1	RC_AA430184_s	Human putative ATP/GTP-binding protein (HEAB) mRNA; complete cds
3	RC_AA431288_s	CD3D antigen; delta polypeptide (TiT3 complex)
1	RC_AA431293	ESTs
3	RC_AA431478	ESTs
3	RC_AA431492	EST
1	RC_AA431732	EST
3	RC_AA432278	EST
4	RC_AA434411	ESTs
3	RC_AA435512_i	ESTs
1	RC_AA435698	ESTs
1	RC_AA435711	Homo sapiens mRNA for KIAA712 protein; complete cds
3	RC_AA435815_s	Clk-associating RS-cyclophilin
3	RC_AA435842	ESTs
3	RC_AA436475	ESTs
3	RC_AA436489	ESTs
3	RC_AA442060	ESTs
1	RC_AA442079	EST
3	RC_AA443151	ESTs
4	RC_AA446133	ESTs
1	RC_AA447145	Homo sapiens KIAA399 mRNA; partial cds
3	RC_AA447398	EST
1	RC_AA447643	ESTs
1	RC_AA447742_s	dynein; axonemal; heavy polypeptide 17-like
3	RC_AA448226	zw96c1.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:784818 3', mRNA sequence
1	RC_AA448825	EST
1	RC_AA449444	ESTs
3	RC_AA450087	regulator of Gz-selective protein signaling

Cluster	Accession # / PROBESET	Gene Description
3	RC_AA450211	EST
1	RC_AA450244	ESTs
3	RC_AA452123	ESTs; Weakly similar to Tcp-1 [M.musculus]
3	RC_AA452155	zinc finger protein 198
3	RC_AA452156	EST
3	RC_AA453036	ESTs
3	RC_AA453526	ESTs
3	RC_AA454085	EST
3	RC_AA454103	ESTs
1	RC_AA454642	ESTs
1	RC_AA454935	ESTs
3	RC_AA456323	ESTs
3	RC_AA457395	EST
3	RC_AA458850	aa26c7.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:81438 3' similar to contains L1.t3 L1 repetitive element ;, mRNA sequence
3	RC_AA459662	EST
3	RC_AA459668	Homo sapiens 3-hydroxyisobutyryl-coenzyme A hydrolase mRNA; complete cds
1	RC_AA459679_s	ESTs; Weakly similar to The KIAA191 gene is expressed ubiquitously. [H.sapiens]
1	RC_AA459702	ESTs
4	RC_AA460017_f	ESTs
3	RC_AA460324	ESTs
3	RC_AA461509	ESTs; Weakly similar to hypothetical protein II [H.sapiens]
3	RC_AA464414_i	ESTs
1	RC_AA464428	ESTs
3	RC_AA470084	ESTs
3	RC_AA476606_s	ESTs
3	RC_AA478521	ESTs
3	RC_AA478523	ESTs; Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]
3	RC_AA479949	ESTs
3	RC_AA481252	RAS-LIKE PROTEIN TC21
1	RC_AA485351	ESTs; Weakly similar to predicted using Genefinder [C.elegans]
1	RC_AA487264	ESTs
1	RC_AA489072	Homo sapiens mRNA for KIAA87 protein; complete cds
1	RC_AA489630	Homo sapiens mRNA for KIAA665 protein; complete cds
2	RC_AA490225	ESTs
3	RC_AA490227	ESTs
3	RC_AA490255	ESTs
1	RC_AA490890	ESTs
2	RC_AA490916_s	ESTs
3	RC_AA490925	Homo sapiens laforin (EPM2A) mRNA; partial cds

Cluster	Accession # / PROBESET	Gene Description
1	RC_AA490955	ESTs; Weakly similar to bullous pemphigoid antigen [M.musculus]
1	RC_AA495812	ESTs
3	RC_AA495824	ESTs
1	RC_AA496369	ESTs
3	RC_AA504125_s	ESTs
1	RC_AA521473	Human brain secretory protein hSec1p (HSEC1) mRNA; complete cds
1	RC_AA598440	ESTs
3	RC_AA598899_i	ESTs
3	RC_AA599244	Homo sapiens mRNA for KIAA53 protein; partial cds
1	RC_AA599694_s	Human mRNA for KIAA133 gene; complete cds
1	RC_AA600037	ESTs
3	RC_AA609135	EST
1	RC_AA609582	Homo sapiens p6 katanin mRNA; complete cds
3	RC_AA609684	ESTs
3	RC_AA609839	ESTs
1	RC_AA609862	Homo sapiens mRNA for RBP-MS/type 3; complete cds
4	RC_AA620423	EST
3	RC_AA620747	EST
1	RC_AA621364	ESTs
2	RC_C20653	ESTs
3	RC_D20085	ESTs
1	RC_D20749	ESTs
2	RC_D51285_s	ESTs
4	RC_D59972_i	ESTs
4	RC_F04112_f	ESTs
2	RC_F13604	ESTs
1	RC_H01662	ESTs
1	RC_H05135_i	ESTs
3	RC_H12245	splicing factor; arginine/serine-rich 7 (35kD)
1	RC_H22842	EST
1	RC_H30894	ESTs
2	RC_H43442_s	Human mRNA for KIAA28 gene; partial cds
3	RC_H45996	ESTs
2	RC_H69281_i	ESTs
3	RC_H69485_f	ESTs
1	RC_H69899	ESTs; Moderately similar to unknown [H.sapiens]
4	RC_H70627_s	ESTs
1	RC_H73050_s	Rhesus blood group; D antigen
1	RC_H73260	ESTs
1	RC_H77531_s	HIR (histone cell cycle regulation defective; S. cerevisiae) homolog A
2	RC_H80552	EST
4	RC_H80737_s	lysyl oxidase
1	RC_H93412	ESTs
3	RC_H94892_s	v-ral simian leukemia viral oncogene homolog A (ras related)

Cluster	Accession # / PROBESET	Gene Description
4	RC_H95643_s	neurotrophic tyrosine kinase; receptor; type 1
2	RC_H96552	ESTs
4	RC_H97146	ESTs; Highly similar to G protein-coupled receptor kinase 6; splice variant B [H.sapiens]
2	RC_H99131_s	ESTs
1	RC_H99462_s	ribosomal protein; mitochondrial; L12
1	RC_H99837_s	ESTs
2	RC_N22140	ESTs; Highly similar to TUBULIN GAMMA CHAIN [Euplotes octocarinatus]
2	RC_N22197	ESTs
1	RC_N23756_s	Human mRNA for KIAA238 gene; partial cds
2	RC_N24134	eukaryotic translation initiation factor 1A; Y chromosome
4	RC_N24195	Homo sapiens mRNA for RanBPM; complete cds
1	RC_N26739	CAAX box 1
2	RC_N27098	EST
1	RC_N27637	ESTs
4	RC_N33090	ESTs; Weakly similar to translation initiation factor [H.sapiens]
1	RC_N35967	ESTs
1	RC_N38959_f	Homo sapiens chaperonin containing t-complex polypeptide 1; beta subunit (Cctb) mRNA; complete cds
2	RC_N39069	ESTs
1	RC_N46441	ESTs
2	RC_N48270_f	ESTs
2	RC_N48365_s	ESTs
2	RC_N51316	ESTs
1	RC_N51499_s	ESTs
4	RC_N53976	ESTs
2	RC_N54157	ESTs
2	RC_N54300	ESTs
1	RC_N54831	ESTs; Weakly similar to neuronal thread protein AD7c-NTP [H.sapiens]
2	RC_N59849	ESTs
4	RC_N62132	ESTs
1	RC_N62375	EST
4	RC_N63138	ESTs
1	RC_N63172	cell division cycle 42 (GTP-binding protein; 25kD)
2	RC_N63772	Homo sapiens DNA sequence from PAC 434O14 on chromosome 1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1; the ADORA2BP adenosine A2b receptor LIKE pseudogene; the IRF
2	RC_N63787	ESTs
2	RC_N68168	za11c1.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:292224 3', mRNA sequence
2	RC_N68201	ESTs; Weakly similar to hypothetical protein [H.sapiens]
2	RC_N68300	ESTs

Cluster	Accession # / PROBESET	Gene Description
1	RC_N68321	solute carrier family 2 (facilitated glucose transporter); member 3
2	RC_N69575	EST
2	RC_N75007	ESTs
1	RC_N75542	ESTs
2	RC_N90066	Homo sapiens clone 24689 mRNA sequence
1	RC_N91246	ESTs
1	RC_N92751	ESTs; Weakly similar to cyclic nucleotide-gated channel beta subunit [R.norvegicus]
2	RC_N93214_s	ESTs
2	RC_N99148	ESTs; Highly similar to MKR2 PROTEIN [Mus musculus]
4	RC_R07876	ESTs; Weakly similar to HYPOTHETICAL PROTEIN HI1723 [Haemophilus influenzae]
1	RC_R10865_f	alpha-fetoprotein
2	RC_R11056	ESTs
2	RC_R11488	ESTs
1	RC_R22947	ESTs
2	RC_R23930_s	ESTs
1	RC_R26589_f	ESTs
4	RC_R37588_s	GDS-related protein
2	RC_R37613	ESTs
1	RC_R38398	Homo sapiens clone 23758 mRNA sequence
2	RC_R39179_f	ESTs
1	RC_R40923	ESTs
1	RC_R41179	Human mRNA for KIAA328 gene; partial cds
2	RC_R41294_s	ESTs
1	RC_R42307_f	early development regulator 2 (homolog of polyhomeotic 2)
1	RC_R43189_f	EST
3	RC_R43306	ESTs
1	RC_R44357	ESTs
1	RC_R44519	EST; Moderately similar to Pro-Pol-dUTPase polyprotein [M.musculus]
2	RC_R45088	yg38g4.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:34896 3', mRNA sequence
2	RC_R47948_i	ESTs
1	RC_R51524	ESTs
1	RC_R54950	ESTs
1	RC_R55241	EST
1	RC_R59585	ESTs
1	RC_R60044	ESTs
2	RC_R60872	ESTs
1	RC_R66690	ESTs
2	RC_R67266_s	exostoses (multiple)-like 1
1	RC_R73588	ESTs
3	RC_R79403	ESTs

Cluster	Accession #/ PROBESET	Gene Description
1	RC_R87647	ESTs
2	RC_R93622	ESTs
4	RC_R99599_s	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)
4	RC_R99612	ESTs
1	RC_T02888	FB14D6 Fetal brain, Stratagene Homo sapiens cDNA clone FB14D6 3'end, mRNA sequence
1	RC_T03170	EST
2	RC_T10465	hbc313 Human pancreatic islet Homo sapiens cDNA clone hbc313 3'end, mRNA sequence
1	RC_T15418_f	ESTs
1	RC_T15597_f	Homo sapiens mRNA for KIAA661 protein; complete cds
2	RC_T15652_i	ESTs
2	RC_T16898_s	ash2 (absent; small; or homeotic; Drosophila; homolog)-like
1	RC_T26644_i	ESTs; Weakly similar to zinc finger protein ZNF139 [H.sapiens]
2	RC_T40841	ESTs
1	RC_T47566_i	yb15c11.s1 Stratagene placenta (#937225) Homo sapiens cDNA clone IMAGE:71252 3' similar to similar to gb:Z2157 ELONGATION FACTOR 1-DELTA (HUMAN), mRNA sequence
2	RC_T50116	ESTs; Moderately similar to EA22 GENE PROTEIN [Bacteriophage lambda]
2	RC_T50145_s	FSHD region gene 1
2	RC_T58615	ESTs; Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]
1	RC_T59940_f	ESTs
4	RC_T63595	ESTs
2	RC_T64891	yd1c2.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:66722 3', mRNA sequence
2	RC_T64924	ESTs
2	RC_T64933_r	ESTs; Weakly similar to hypothetical protein [H.sapiens]
2	RC_T68875	yc3f5.s1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:8229 3', mRNA sequence
2	RC_T69027	ESTs
3	RC_T69924	yc19d3.s1 Stratagene lung (#93721) Homo sapiens cDNA clone IMAGE:81125 3', mRNA sequence
3	RC_T70353	ESTs
1	RC_T79780_s	ESTs; Weakly similar to PUTATIVE MITOCHONDRIAL CARRIER YBR291C [Saccharomyces cerevisiae]
2	RC_T79951	ESTs
3	RC_T80174_s	ESTs
3	RC_T80622	ESTs; Weakly similar to envelope protein RIC-7 [H.sapiens]
1	RC_T85352	ESTs
1	RC_T85373	ESTs

Cluster	Accession # / PROBESET	Gene Description
2	RC_T86284	ESTs; Weakly similar to transformation-related protein [H.sapiens]
1	RC_T89579_s	Homo sapiens E2F-related transcription factor (DP-1) mRNA; complete cds
3	RC_T90360	ESTs
2	RC_T94328_i	ESTs
1	RC_T95590	ye4a3.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:12172 3' similar to gb|M1817|IGURRAA Iguana iguana 5S (rRNA);, mRNA sequence
4	RC_T97257_f	ESTs; Weakly similar to hypothetical protein [H.sapiens]
2	RC_T97599_i	ESTs
2	RC_T97620	ESTs; Weakly similar to unknown [H.sapiens]
4	RC_T97775	ESTs
3	RC_T98152	fibrillin 2
1	RC_W31479	ESTs
1	RC_W37999	ESTs
2	RC_W38240	Accession not listed in Genbank
2	RC_W40150	human chromosome-associated polypeptide (barnacan)
2	RC_W45435	Homo sapiens mRNA for KIAA784 protein; partial cds
2	RC_W58202	ESTs
1	RC_W58344	ESTs
2	RC_W58650	ESTs
4	RC_W68736	Human DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3; EC 1.6.99.3; CI-MLRQ); Tubulin Beta and Proto-oncogene Tyrosine-protein
2	RC_W69106	ESTs
2	RC_W69111	ESTs
1	RC_W69385_s	H.sapiens NuMA gene (Clone T33)
3	RC_W69399_s	ATPase; Ca++ transporting; plasma membrane 1
3	RC_W69459	ESTs
2	RC_W72424	S1 calcium-binding protein A9 (calgranulin B)
2	RC_W72724	ESTs
2	RC_W72834	ESTs
1	RC_W73955	Homo sapiens chromosome 19; cosmid R26445
2	RC_W74701	ESTs
2	RC_W76540	ESTs
2	RC_W79397	ESTs
2	RC_W85888	ESTs; Weakly similar to synapse associated protein sap47-2 [D.melanogaster]
2	RC_W86038	ESTs
2	RC_W86881	ESTs
2	RC_W87804	ESTs
2	RC_W88942	zh7b5.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:417393 3', mRNA sequence

Cluster	Accession # / PROBESET	Gene Description
3	RC_W90022	ESTs; Highly similar to LECT2 precursor [H.sapiens]
2	RC_W92272	Homo sapiens zinc-finger helicase (hZFH) mRNA; complete cds
2	RC_W92764_s	TUMOR NECROSIS FACTOR-INDUCIBLE PROTEIN TSG-6 PRECURSOR
2	RC_W93040	ESTs
3	RC_W93092	neutral sphingomyelinase (N-SMase) activation associated factor
2	RC_W93227	EST
2	RC_W93523	ESTs
2	RC_W93659	ESTs
2	RC_W94003_s	ESTs
2	RC_W94401_s	ESTs
2	RC_W94688	Homo sapiens mRNA for perilipin; complete cds
2	RC_W94787_s	ESTs
2	RC_Z38294_s	ESTs
3	RC_Z38311	ESTs
2	RC_Z38465_s	ESTs
2	RC_Z38525_s	ESTs
2	RC_Z38538_f	ESTs
2	RC_Z38551_s	ESTs
2	RC_Z38783_s	ca2+-dependent activator protein for secretion; Ca2+-regulated cytoskeletal protein (CAPS)
2	RC_Z39113	ESTs
4	RC_Z39255_f	ESTs
2	RC_Z39591	EST
2	RC_Z39783_s	ESTs
2	RC_Z39920	ESTs; Highly similar to NADH-CYTOCHROME B5 REDUCTASE [Bos taurus]
2	RC_Z40166_f	ESTs
3	RC_Z40388_s	ESTs
2	RC_Z40646	ESTs
2	RC_Z41697	ESTs
2	RC_Z99349	ESTs
2	RC_Z99394_s	ESTs; Weakly similar to transformation-related protein [H.sapiens]

Table 2

PROBESET	Accession	Complete Title	SS1(Psort)	SS2(Psort)	TM1(Psort)	TM2(Psort)	MainType(Psort)	SubType(Psort)
EOS33789	1_U86782	26S proteasome-associated pad1 homolog	N	N			N	
EOS30212	1_X55740	5' nucleotidase (CD73)	Y	Y	Type Ia	YType Ia		
EOS19489	C_RC_W38197	Accession not listed in Genbank						
EOS33608	1_K02574	Accession not listed in Genbank						
EOS01114	1_L19871	activating transcription factor 3	N	N			N	
EOS33514	1_D90209	activating transcription factor 4 (tax-responsive enha	N	N			N	
EOS00098	1_D14874	adrenomedullin	Y	N			N	
EOS33456	1_M11313	alpha-2-macroglobulin	Y	N			N	
EOS33029	1_L09209	amyloid beta (A4) precursor-like protein 2	N	N			N	
EOS01435	1_M27396	asparagine synthetase	N	N			N	
EOS02429	1_U51478	ATPase; Na+/K+ transporting; beta 3 polypeptide	N	Y	Type II (Ncyt	YType II (Ncyt Cexo)		
EOS06564	A_RC_AA459916	bradykinin receptor B2	N	N			N	
EOS02490	1_U59289	cadherin 13; H-cadherin (heart)	Y	Y	Type Ia	YType Ia		
EOS01275	1_L76380	calcitonin receptor-like	Y	Y	Type IIIa (clv	YType IIIa (clv)		
EOS00459	1_HG1862-HT1897	Calmodulin Type I						
EOS30361	1_L10284	calnexin	Y	Y	Type Ia	YType Ia		
EOS01405	1_M23254	calpain; large polypeptide L2	N	N			N	
EOS24693	D_RC_R39610_s	calpain; large polypeptide L2	N	N			N	
EOS34311	1_U56637	capping protein (actin filament) muscle Z-line; alpha	N	N			N	
EOS24656	D_RC_R15740	carbohydrate (chondroitin 6/keratan) sulfotransferas	Y	N			N	
EOS25539	N_134_2	carbohydrate (chondroitin 6/keratan) sulfotransferas	N	Y	Type II (Ncyt	YType II (Ncyt Cexo)		
EOS32646	B_RC_T35289	casein kinase 1; alpha 1	N	N			N	
EOS01943	1_U03100	catenin (cadherin-associated protein); alpha 1 (102k	N	N			N	
EOS03277	1_X87838	catenin (cadherin-associated protein); beta 1 (88kD)	N	N			N	
EOS00780	1_HG417-HT417	Cathepsin B						
EOS34488	1_S53911	CD34	Y	Y	Type Ia	YType Ia		
EOS01723	1_M84349	CD59 antigen p18-20 (antigen identified by monoclo	Y	N			N	
EOS34423	1_X15183	CDW52 antigen (CAMPATH-1 antigen)	N	N			N	
EOS01027	1_L06797	chemokine (C-X-C motif); receptor 4 (fusin)	N	Y	Type IIIb (Ne	YType IIIb (Nexo Ccyt)		
EOS00548	1_HG2814-HT2710	Collagen, Type VIII, Alpha 1						
EOS01426	1_M26576_cds2	collagen; type IV; alpha 1	Y	N			N	
EOS01768	1_M92934	connective tissue growth factor	N	Y	Type Ib (Nex	YType Ib (Nexo Ccyt)		
EOS29428	D_RC_AA449789_f	connective tissue growth factor						
EOS03010	1_X59798	cyclin D1 (PRAD1: parathyroid adenomatosis 1)	N	N			N	

Table 2, cont.

EOS33328	1_X02612	cytochrome P450; subfamily I (aromatic compound-I	Y	Type Ib (Nex YType Ib (Nexo Ccyt)
EOS24269	D_RC_H99093	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide (72kD)		N
EOS02890	1_X15729	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 5 (	N	Y
EOS01896	1_S81914	DIFFERENTIATION-DEPENDENT GENE 2	N	Y Type II (Ncyt YType II (Ncyt Cexo)
EOS33581	1_U97105	dihydropyrimidinase-like 2	N	N
EOS34133	1_M60278	diphtheria toxin receptor (heparin-binding epidermal	Y	Y Type Ia YType Ia
EOS34269	A_RC_AA478971_s	disabled (Drosophila) homolog 2 (mitogen-responsiv	N	N
EOS29195	1_X68277	dual specificity phosphatase 1	N	N
EOS32233	C_RC_AA620962	dynein; cytoplasmic; light intermediate polypeptide 2	Y	N
EOS02230	1_U32944	dynein; cytoplasmic; light polypeptide	N	N
EOS02941	1_X52541	early growth response 1	N	N
EOS01954	1_U03877	EGF-containing fibulin-like extracellular matrix protei	N	Y Type II (Ncyt YType II (Ncyt Cexo)
EOS31010	1_J05008	endothelin 1	Y	N
EOS28572	1_L35240 A_L3524	enigma (LIM domain protein)	N	N
EOS01563	1_M57730	ephrin-A1	Y	Y Type Ib (Nex YType Ib (Nexo Ccyt)
EOS03897	A_AA303711	ephrin-B1	Y	Y Type Ia YType Ia
EOS21265	D_RC_AA404418	EST		
EOS04377	A_L44538	ESTs	N	N
EOS04694	A_RC_AA025351	ESTs	N	N
EOS04713	A_RC_AA027050	ESTs	Y	Y Type Ib (Nex YType Ib (Nexo Ccyt)
EOS04728	A_RC_AA029462	ESTs	N	N
EOS04795	A_RC_AA045136	ESTs	N	N
EOS04807	A_RC_AA047437	ESTs	N	N
EOS05108	A_RC_AA187490	ESTs	N	N
EOS05145	A_RC_AA205724	ESTs	N	N
EOS05193	A_RC_AA227926	ESTs	N	N
EOS05201	A_RC_AA227986	ESTs	N	N
EOS05260	A_RC_AA234743	ESTs	N	N
EOS05391	A_RC_AA253216	ESTs	N	N
EOS05423	A_RC_AA256268	ESTs	N	N
EOS05697	A_RC_AA346551	ESTs	N	N
EOS05812	A_RC_AA400292	ESTs	N	N
EOS05866	A_RC_AA404338	ESTs	N	N
EOS06054	A_RC_AA423987	ESTs	N	N
EOS06152	A_RC_AA428594	ESTs	N	N

Table 2, cont.

EOS06171	A_RC_AA430108	ESTs	N	N		N	
EOS06193	A_RC_AA431462	ESTs	N	N		N	
EOS06654	A_RC_AA465226	ESTs	N	N		N	
EOS06723	A_RC_AA478778	ESTs	N	N		N	
EOS06729	A_RC_AA479037	ESTs	Y	N		N	
EOS06891	A_RC_AA504110	ESTs	N	N		N	
EOS06960	A_RC_AA599434	ESTs	N	Y	Type II (Ncyt	Y	Type II (Ncyt Cexo)
EOS07016	A_RC_AA609519	ESTs	N	N		N	
EOS08437	B_RC_AA083514	ESTs	N	Y	Type II (Ncyt	Y	Type II (Ncyt Cexo)
EOS08625	B_RC_AA121315	ESTs	Y	N		N	
EOS08861	B_RC_AA147186	ESTs					
EOS08931	B_RC_AA156125	ESTs	N	N		N	
EOS09125	B_RC_AA188932	ESTs	N	N		N	
EOS09320	B_RC_AA219653	ESTs	N	N		N	
EOS09386	B_RC_AA232645	ESTs	N	N		N	
EOS09667	B_RC_F10078	ESTs	N	N		N	
EOS10341	B_RC_H48032	ESTs	N	N		N	
EOS10590	B_RC_H82117	ESTs	N	N		N	
EOS10836	B_RC_N39584	ESTs	N	N		N	
EOS11021	B_RC_N59858	ESTs	N	N		N	
EOS11286	B_RC_N90933	ESTs	Y	N		N	
EOS11671	B_RC_R26124	ESTs	N	N		N	
EOS11699	B_RC_R27957	ESTs	N	N		N	
EOS13420	B_RC_T88700	ESTs	N	N		N	
EOS13472	B_RC_T90527	ESTs	N	N		N	
EOS13733	B_RC_W42789	ESTs	N	N		N	
EOS13840	B_RC_W78175	ESTs	N	N		N	
EOS13877	B_RC_W84768	ESTs					
EOS14991	C_RC_AA253217	ESTs	N	N		N	
EOS15749	C_RC_AA426573	ESTs	N	Y	Type II (Ncyt	Y	Type II (Ncyt Cexo)
EOS15800	C_RC_AA432374	ESTs	N	N		N	
EOS15894	C_RC_AA446622	ESTs	N	N		N	
EOS16158	C_RC_AA478771	ESTs	N	N		N	
EOS16194	C_RC_AA482594	ESTs	N	N		N	
EOS16244	C_RC_AA490588	ESTs	N	N		N	

Table 2, cont.

EOS16519	C_RC_D59570_f	ESTs	Y	Y	Y	Type II (Ncyt	YType II (Ncyt Cexo)			
EOS16953	C_RC_H88157	ESTs	N	Y	Y	Type II (Ncyt	YType II (Ncyt Cexo)			
EOS17042	C_RC_H94648	ESTs	N	N	N		N			
EOS17086	C_RC_H97538	ESTs	N	N	N		N			
EOS20585	D_RC_AA287347	ESTs	N	N	N		N			
EOS21244	D_RC_AA402799	ESTs	N	N	N		N			
EOS21752	D_RC_AA425107	ESTs	N	N	N		N			
EOS22261	D_RC_AA442872	ESTs	Y	N	N		N			
EOS23989	D_RC_F13673	ESTs	N	N	N		N			
EOS25097	D_RC_W45560	ESTs	N	N	N		N			
EOS25237	D_RC_Z40583_f	ESTs	N	N	N		N			
EOS25259	N_101234_4	ESTs	N	Y	N	Type II (Ncyt	YType II (Ncyt Cexo)			
EOS27365	N_62063_2	ESTs	N	N	N		N			
EOS27496	N_665011_1	ESTs	N	Y	N	Type Ib (Nex	YType Ib (Nexo Ccyt)			
EOS27549	N_682558_1	ESTs	N	N	N		N			
EOS28833	A_R69417	ESTs	N	N	N		N			
EOS29017	B_RC_N72695_s	ESTs	N	N	N		N			
EOS29418	A_AA228107	ESTs	N	N	N		N			
EOS29487	A_W01367_s B_RC	ESTs		N	N		N			
EOS30568	C_RC_H16402	ESTs	N	Y	Y	Type II (Ncyt	YType II (Ncyt Cexo)			
EOS30569	C_RC_D59711_f	ESTs	Y	N	N		N			
EOS30616	A_RC_AA431571	ESTs	N	N	N		N			
EOS30748	A_RC_AA280375 C	ESTs	N	N	N		N			
EOS30829	B_RC_Z41740_s	ESTs	N	Y	N		N			
EOS31014	A_RC_AA101878	ESTs	Y	N	N		N			
EOS31037	A_N87590	ESTs	N	N	N		N			
EOS31112	A_RC_AA256153_i	ESTs	N	N	N		N			
EOS31494	A_RC_AA491465	ESTs	N	N	N		N			
EOS31503	A_AA046593 A_RC	ESTs	N	N	N		N			
EOS31686	A_D45304 D_RC_N	ESTs	N	N	N		N			
EOS31978	A_AA384503_s	ESTs	N	N	N		N			
EOS31980	A_AA136353	ESTs	N	N	N		N			
EOS32328	A_R31641	ESTs	N	N	N		N			
EOS32351	C_RC_AA489190	ESTs	Y	Y	Y	Type Ib (Nex	YType Ib (Nexo Ccyt)			
EOS32813	A_AA047151 A_RC	ESTs	N	N	N		N			

Table 2, cont.

EOS32919	A_AA480074	ESTs	N	N	N		
EOS33001	B_RC_T99789	ESTs	N	N	N		
EOS33079	B_RC_T16484_s	ESTs	N	N	N		
EOS33091	A_RC_AA253193	ESTs	Y	N	N		
EOS33130	A_RC_AA432248 D	ESTs	N	N	N		
EOS33279	A_N75791_s A_RC	ESTs	N	N	N		
EOS33440	B_RC_AA227913 C	ESTs	N	N	N		
EOS33819	A_AA099391_s B_	ESTs	N	N	N		
EOS34229	A_RC_AA487558 A	ESTs	N	N	N		
EOS34992	A_AA174183_s	ESTs	N	N	N		
EOS35003	A_AA452000 C_RC	ESTs	N	N	N		
EOS35100	A_RC_AA282140 A	ESTs	N	N	N		
EOS31845	A_AA316186 A_RC	ESTs; Highly similar to (defline not available 426213	N	N	N		
EOS29549	A_RC_AA610116_J	ESTs; Highly similar to (defline not available 432518	N	Y	N	Type IIIa (Nc	YType IIIa (Ncyt Cexo)
EOS31021	A_T35341_s	ESTs; Highly similar to (defline not available 451988	N	N	N		
EOS06772	A_RC_AA482597	ESTs; Highly similar to (defline not available 470473	N	N	N		
EOS06384	A_RC_AA449479	ESTs; Highly similar to (defline not available 510678	Y	N	N		
EOS06798	A_RC_AA487561	ESTs; Highly similar to RAS-RELATED PROTEIN R	N	N	N		
EOS06904	A_RC_AA520989	ESTs; Highly similar to SERINE/THREONINE PRO	N	N	N		
EOS28445	A_RC_AA149044	ESTs; Highly similar to the KIAA0195 gene is expre	Y	N	N		
EOS12881	B_RC_T16550	ESTs; Highly similar to vacuolar protein sorting hom	N	N	N		
EOS11308	B_RC_N93764	ESTs; Moderately similar to !!!! ALU CLASS C WAR	Y	Y	N	Type Ib (Nex	YType Ib (Nexo Ccyt)
EOS21765	D_RC_AA425435	ESTs; Moderately similar to !!!! ALU SUBFAMILY J	N	N	N		
EOS19796	C_RC_W80814	ESTs; Moderately similar to !!!! ALU SUBFAMILY S	N	N	N		
EOS04882	A_RC_AA071089	ESTs; Moderately similar to !!!! ALU SUBFAMILY S	Y	N	N		
EOS17210	C_RC_N22107	ESTs; Moderately similar to !!!! ALU SUBFAMILY S	N	N	N		
EOS22507	D_RC_AA452860	ESTs; Moderately similar to !!!! ALU SUBFAMILY S	N	N	N		
EOS05657	A_RC_AA292379	ESTs; Moderately similar to !!!! ALU SUBFAMILY S	N	N	N		
EOS23090	D_RC_AA488687	ESTs; Moderately similar to !!!! ALU SUBFAMILY S	Y	N	N		
EOS06296	A_RC_AA443756	ESTs; Moderately similar to (defline not available 41	N	N	N		
EOS28553	A_D78676 D_RC_A	ESTs; Moderately similar to (defline not available 45	N	N	N		
EOS05524	A_RC_AA279397	ESTs; Moderately similar to fibronectin [H.sapiens]	N	N	N		
EOS12248	B_RC_R55470	ESTs; Moderately similar to K02E10.2 [C.elegans]	N	N	N		
EOS05126	A_RC_AA195031	ESTs; Moderately similar to PROBABLE G PROTEI	N	N	N		
EOS34919	A_AA236324 B_RC	ESTs; Weakly similar to !!!! ALU CLASS A WARNIN	Y	N	N		

Table 2, cont.

EOS34999	C_RC_AA456311_s	ESTs; Weakly similar to !!!! ALU CLASS A WARNIN Y	N		N	
EOS32081	A_AA044755_s D_	ESTs; Weakly similar to !!!! ALU SUBFAMILY SX W N	N		N	
EOS17106	C_RC_H98670	ESTs; Weakly similar to (defline not available 48840 N	N		N	
EOS06194	A_RC_AA431470	ESTs; Weakly similar to CAMP-DEPENDENT PRO N	N		N	
EOS28844	A_AA232837	ESTs; Weakly similar to Human pre-mRNA cleavag Y	Y	Type II (Ncyt	YType II (Ncyt Cexo)	
EOS05662	A_RC_AA292717	ESTs; Weakly similar to JM2 [H.sapiens] N	N		N	
EOS32117	A_RC_AA058911	ESTs; Weakly similar to membrane glycoprotein [M. N	Y	Type II (Ncyt	YType II (Ncyt Cexo)	
EOS13977	B_RC_W94427	ESTs; Weakly similar to Na;K-ATPase gamma subu Y	Y	Type Ia	YType Ia	
EOS12987	B_RC_T26674	ESTs; Weakly similar to neuronal thread protein AD N	N		N	
EOS23416	D_RC_AA599674	ESTs; Weakly similar to ORF [D.melanogaster] N	N		N	
EOS32540	A_RC_AA443114	ESTs; Weakly similar to PIM-1 PROTO-ONCOGEN N	N		N	
EOS05043	A_RC_AA156450	ESTs; Weakly similar to Similar to Rat trg gene prod N	N		N	
EOS06820	A_RC_AA489245	ESTs; Weakly similar to sperm specific protein [H.sapiens]				
EOS31839	D_RC_W69127_s	ESTs; Weakly similar to zinc finger protein ZNF191 [N	N		N	
EOS03125	1_X70940	eukaryotic translation elongation factor 1 alpha 2 N	N		N	
EOS02623	1_U73824	eukaryotic translation initiation factor 4 gamma; 2 N	N		N	
EOS01787	1_M94856	fatty acid binding protein 5 (psoriasis-associated) N	N		N	
EOS28383	1_X02761	fibronectin 1 N	N		N	
EOS00606	1_HG3044-HT3742	Fibronectin, Alt. Splice 1				
EOS02950	1_X53416	filamin A; alpha (actin-binding protein-280) N	Y	Type II (Ncyt	YType II (Ncyt Cexo)	
EOS01612	1_M62994	filamin B; beta (actin-binding protein-278) N	N		N	
EOS01247	1_L42176	four and a half LIM domains 2 N	N		N	
EOS33732	1_L16862 A_RC_A	G protein-coupled receptor kinase 6 N	N		N	
EOS33447	1_X52947	gap junction protein; alpha 1; 43kD (connexin 43) N	Y	Type IIIa (Nc	YType IIIa (Ncyt Cexo)	
EOS02812	1_X04412	gelsolin (amyloidosis; Finnish type) N	N		N	
EOS02959	1_X54489_ma1	GRO1 oncogene (melanoma growth stimulating acti N	Y	Type II (Ncyt	YType II (Ncyt Cexo)	
EOS01564	1_M57731	GRO2 oncogene N	Y	Type II (Ncyt	YType II (Ncyt Cexo)	
EOS02213	1_U31384	guanine nucleotide binding protein 11 N	N		N	
EOS33321	1_X57579 C_RC_N	H.sapiens activin beta-A subunit (exon 2) Y	N		N	
EOS33408	A_X83703 D_RC_A	H.sapiens mRNA for cytokine inducible nuclear prot N	N		N	
EOS25234	D_RC_Z39833	H.sapiens mRNA for Rho6 protein N	N		N	
EOS33601	D_RC_T25747_s	H.sapiens OZF mRNA				
EOS03362	1_X97748	H.sapiens PTX3 gene promotor region				
EOS03068	1_X65965	H.sapiens SOD-2 gene for manganese superoxide dismutase				
EOS32288	1_X60486	H4 histone family; member G N	N		N	

Table 2, cont.

EOS00588	1_HG2855-HT2995	Heat Shock Protein, 70 Kda (Gb:Y00371)			N			N	
EOS35001	1_L08069	heat shock protein; DNAJ-like 2	N	N	Y	Type II (Ncyt	YType II (Ncyt Cexo)		
EOS02837	1_X06985	heme oxygenase (decycling) 1	N	N	N			N	
EOS01674	1_M75126	hexokinase 1	N	N	N				
EOS01487	1_M31994	Homo sapiens aldehyde dehydrogenase (ALDH1) gene, exon 13 and complete cds							
EOS32770	A_N23817 A_RC_A	Homo sapiens clone 23675 mRNA sequence	N	N	Y	Type Ib (Nex	YType Ib (Nexo Ccyt)		
EOS33421	1_L40395 A_L4039	Homo sapiens clone 23689 mRNA; complete cds	N	N	N			N	
EOS06991	A_RC_AA608649	Homo sapiens clone 23742 mRNA; partial cds	Y	Y	Y	Type Ia	YType Ia		
EOS02519	1_U62015	Homo sapiens Cyr61 mRNA, complete cds	Y	N	N			N	
EOS00044	1_D00596	Homo sapiens gene for thymidylate synthase; exons N		N	N			N	
EOS33755	1_U44975	Homo sapiens Kruppel-like zinc finger protein Zf9 m N		N	N			N	
EOS34982	B_RC_AA148923	Homo sapiens mRNA for DEPP (decidual protein in N		N	N			N	
EOS29692	A_RC_AA460273 A	Homo sapiens mRNA for KIAA0517 protein; partial c N		N	N			N	
EOS30706	A_R79356	Homo sapiens mRNA for KIAA0544 protein; partial c N		N	N			N	
EOS30932	A_RC_AA121543 D	Homo sapiens mRNA for KIAA0758 protein; partial c Y		N	N			N	
EOS31137	B_RC_W74533 D_	Homo sapiens mRNA for KIAA0786 protein; partial c Y		N	N			N	
EOS32898	A_N77151 C_RC_A	Homo sapiens mRNA for KIAA0799 protein; partial c N		N	N			N	
EOS00335	1_D86425	Homo sapiens mRNA for nidogen-2	Y	N	N			N	
EOS10948	B_RC_N54067	Homo sapiens mRNA for NIK; partial cds							
EOS07915	B_RC_AA035638	Homo sapiens mRNA; cDNA DKFZp564F053 (from Y		N	N			N	
EOS25528	N_132515_1	Homo sapiens mRNA; cDNA DKFZp564F053 (from Y		N	N			N	
EOS29557	A_RC_AA258308	Homo sapiens mRNA; cDNA DKFZp564F053 (from Y		N	N			N	
EOS02390	1_U48959	Homo sapiens myosin light chain kinase (MLCK) m N		N	N			N	
EOS34333	1_M61199	Human cleavage signal 1 protein mRNA; complete c N		N	N			N	
EOS02617	1_U73379	Human cyclin-selective ubiquitin carrier protein mRN N		N	N			N	
EOS34005	1_U28811	Human cysteine-rich fibroblast growth factor recepto N		N	N			N	
EOS01098	1_L15388	Human G protein-coupled receptor kinase (GRK5) N		N	N			N	
EOS01266	1_L49169	Human G0S3 mRNA; complete cds	N	N	N			N	
EOS02530	1_U63825	Human hepatitis delta antigen interacting protein A (N		N	N			N	
EOS33492	1_M60721	Human homeobox gene, complete cds	Y	N	N			N	
EOS07146	A_RC_D51069_f	Human isolate JuSo MUC18 glycoprotein mRNA (3' variant); complete cds							
EOS01122	1_L20859	Human leukemia virus receptor 1 (GLVR1) mRNA; c N		N	Y	Type IIIa (Nc	YType IIIa (Ncyt Cexo)		
EOS02575	1_U67963	Human lysophospholipase homolog (HU-K5) mRNA; N		N	N			N	
EOS02325	1_U41767	Human metargidin precursor mRNA, complete cds Y		Y	Y	Type Ia	YType Ia		
EOS33547	A_RC_AA148318_s	Human mRNA for KIAA0069 gene; partial cds N		Y	Y	Type IIIa (Nc	YType IIIa (Ncyt Cexo)		

Table 2, cont.

EOS31622	1_D50914	Human mRNA for KIAA0124 gene; partial cds	N	Y	Type II (Ncyt	YType II (Ncyt Cexo)
EOS00350	1_D86983	Human mRNA for KIAA0230 gene; partial cds	Y	N		N
EOS34346	1_M28882 1_X6826	Human MUC18 glycoprotein mRNA, complete cds	Y	Y	Type Ia	YType Ia
EOS02421	1_U51010	Human nicotinamide N-methyltransferase gene, exon 1 and 5' flanking region				
EOS02453	1_U53445	Human ovarian cancer downregulated myosin heavy N		N		N
EOS01644	1_M68874	Human phosphatidylcholine 2-acylhydrolase (cPLA2 N		N		N
EOS02308	1_U40369_ma1	Human spermidine/spermine N1-acetyltransferase (N		N		N
EOS34747	1_U20734 1_X5134	Human transcription factor junB (junB) gene; 5' regio N		N		N
EOS00648	1_HG3342-HT3519	Id1				
EOS33368	D_RC_H44631_s	Immediate early protein	N	N		N
EOS29156	1_M96843 A_M968	inhibitor of DNA binding 2; dominant negative helix-l N		N		N
EOS33768	1_M97796	inhibitor of DNA binding 2; dominant negative helix-l N		N		N
EOS03106	1_X69111	inhibitor of DNA binding 3; dominant negative helix-l N		N		N
EOS02986	1_X57206	inositol 1;4;5-trisphosphate 3-kinase B	N	N		N
EOS00682	1_HG3543-HT3739	Insulin-Like Growth Factor 2				
EOS01517	1_M35878	insulin-like growth factor binding protein 3	Y	N		N
EOS30108	1_M62403	insulin-like growth factor-binding protein 4	Y	N		N
EOS32476	1_M24283 B_RC_A	intercellular adhesion molecule 1 (CD54); human rhi Y		Y	Type Ia	YType Ia
EOS01490	1_M32334	intercellular adhesion molecule 2	Y	Y	Type Ia	YType Ia
EOS31485	A_RC_AA161292_s	interferon; alpha-inducible protein 27	N	Y	Type IIIa (Nc	YType IIIa (Ncyt Cexo)
EOS33077	1_D12763	interleukin 1 receptor-like 1	Y	N		N
EOS32929	1_Y00787	interleukin 8	Y	N		N
EOS32450	C_RC_AA257993	Janus kinase 1 (a protein tyrosine kinase)	N	N		N
EOS31439	1_X56681	jun D proto-oncogene	N	N		N
EOS02857	1_X12876	keratin 18	N	N		N
EOS34262	1_D86962	KIAA0207 gene product	N	N		N
EOS02689	1_U81607	kinase scaffold protein gravin	N	N		N
EOS28599	D_RC_AA598737_s	lactate dehydrogenase B	Y	N		N
EOS33969	1_S78569	laminin; alpha 4	Y	N		N
EOS32420	B_RC_F13782_s C	LIM binding domain 2	N	N		N
EOS33225	1_L00352	low density lipoprotein receptor (familial hypercholes Y		Y	Type Ia	YType Ia
EOS29814	A_RC_AA286710	lymphocyte adaptor protein	N	N		N
EOS02734	1_U89942	lysyl oxidase-like 2	Y	N		N
EOS02494	1_U59423	MAD (mothers against decapentaplegic; Drosophila) N		N		N
EOS28425	A_AF010193	MAD (mothers against decapentaplegic; Drosophila) N		N		N

Table 2, cont.

EOS00073	1_D13640	major histocompatibility complex; class I; C	N	N	
EOS33652	1_X53331	matrix Gla protein	Y	N	
EOS02966	1_X54925	matrix metalloproteinase 1 (interstitial collagenase)	Y	N	
EOS02845	1_X07820	matrix metalloproteinase 10 (stromelysin 2)	Y	N	
EOS29948	B_RC_T68873_f	metallothionein 1L	N	N	
EOS02639	1_U77604	microsomal glutathione S-transferase 2	Y	Y	Type Ia YType Ia
EOS00758	1_HG4069-HT4339	Monocyte Chemotactic Protein 1			Type Ib (Nex YType Ib (Nexo Ccyt)
EOS01040	1_L08246	myeloid cell leukemia sequence 1 (BCL2-related)	Y	Y	N
EOS29275	A_AA292440_s D_	myeloid differentiation primary response	N	N	N
EOS02051	1_U14391	myosin IC	N	N	N
EOS35126	1_J02854	myosin regulatory light chain 2; smooth muscle isofo	N	N	N
EOS24294	D_RC_N23031	myosin; heavy polypeptide 7; cardiac muscle; beta	N	N	N
EOS34094	D_RC_C14407_f D_	neuronal tissue-enriched acidic protein	N	N	N
EOS01989	1_U08021	nicotinamide N-methyltransferase	N	N	N
EOS00385	1_D87953	N-myc downstream regulated	N	N	N
EOS01650	1_M69043	nuclear factor of kappa light polypeptide gene enhan	N	N	N
EOS01597	1_M60858_ma1	nucleolin	N	N	N
EOS05422	A_RC_AA256210	oncomodulin	N	N	N
EOS30077	1_D63476	PAK-interacting exchange factor beta	N	N	N
EOS01473	1_M31166	pentaxin-related gene; rapidly induced by IL-1 beta	Y	N	
EOS00060	1_D11428	peripheral myelin protein 22	Y	Y	Type IIIa (clv YType IIIa (clv)
EOS04824	A_RC_AA054087	phospholipase A2; group IVC (cytosolic; calcium-ind	N	Y	Type Ib (Nex YType Ib (Nexo Ccyt)
EOS35278	A_AA442054_s	phospholipase C; gamma 1 (formerly subtype 148)	Y	N	N
EOS33907	1_L19314	phosphorylase kinase; beta	N	N	N
EOS30483	A_RC_AA430032	pituitary tumor-transforming 1	N	N	N
EOS00921	1_J03764	plasminogen activator inhibitor; type I	N	N	N
EOS13777	B_RC_W60002_s	plastin 3 (T isoform)	N	N	N
EOS07315	A_U97519	podocalyxin-like	N	Y	Type IIIa (Nc YType IIIa (Ncyt Cexo)
EOS05961	A_RC_AA412284_s	poliovirus receptor	Y	N	N
EOS01522	1_M36429	postmeiotic segregation increased 2-like 12	N	N	N
EOS32094	1_U84573	procollagen-lysine; 2-oxoglutarate 5-dioxygenase (ly	N	N	N
EOS07374	A_W28391	proliferation-associated 2G4; 38kD	N	N	N
EOS01086	1_L13977	prolylcarboxypeptidase (angiotensinase C)	Y	N	N
EOS34913	1_D28235 1_U0463	prostaglandin-endoperoxide synthase 2 (prostagland	Y	N	
EOS01770	1_M93056	protease inhibitor 2 (anti-elastase); monocyte/neutro	N	Y	Type Ib (Nex YType Ib (Nexo C

Table 2, cont.

EOS00073	1_D13640	major histocompatibility complex; class I; C	N	N	
EOS33652	1_X53331	matrix Gla protein	Y	N	
EOS02966	1_X54925	matrix metalloproteinase 1 (interstitial collagenase)	Y	N	
EOS02845	1_X07820	matrix metalloproteinase 10 (stromelysin 2)	Y	N	
EOS29948	B_RC_T68873_f	metallothionein 1L	N	N	
EOS02639	1_U77604	microsomal glutathione S-transferase 2	Y	Type Ia	YType Ia
EOS00758	1_HG4069-HT4339	Monocyte Chemotactic Protein 1			
EOS01040	1_L08246	myeloid cell leukemia sequence 1 (BCL2-related)	Y	Type Ib (Nex	YType Ib (Nexo Ccyt)
EOS29275	A_AA292440_s D_	myeloid differentiation primary response	N	N	
EOS02051	1_U14391	myosin IC	N	N	
EOS35126	1_J02854	myosin regulatory light chain 2; smooth muscle isofo	N	N	
EOS24294	D_RC_N23031	myosin; heavy polypeptide 7; cardiac muscle; beta	N	N	
EOS34094	D_RC_C14407_f D_	neuronal tissue-enriched acidic protein	N	N	
EOS01989	1_U08021	nicotinamide N-methyltransferase	N	N	
EOS00385	1_D87953	N-myc downstream regulated	N	N	
EOS01650	1_M69043	nuclear factor of kappa light polypeptide gene enhan	N	N	
EOS01597	1_M60858_ma1	nucleolin	N	N	
EOS05422	A_RC_AA256210	oncomodulin	N	N	
EOS30077	1_D63476	PAK-interacting exchange factor beta	N	N	
EOS01473	1_M31166	pentaxin-related gene; rapidly induced by IL-1 beta	Y	N	
EOS00060	1_D11428	peripheral myelin protein 22	Y	Type IIIa (clv	YType IIIa (clv)
EOS04824	A_RC_AA054087	phospholipase A2; group IVC (cytosolic; calcium-ind	N	Type Ib (Nex	YType Ib (Nexo Ccyt)
EOS35278	A_AA442054_s	phospholipase C; gamma 1 (formerly subtype 148)	Y	N	
EOS33907	1_L19314	phosphorylase kinase; beta	N	N	
EOS30483	A_RC_AA430032	pituitary tumor-transforming 1	N	N	
EOS00921	1_J03764	plasminogen activator inhibitor; type I	N	N	
EOS13777	B_RC_W60002_s	plastin 3 (T isoform)	N	N	
EOS07315	A_U97519	podocalyxin-like	N	Type IIIa (Nc	YType IIIa (Ncyt Cexo)
EOS05961	A_RC_AA412284_s	poliovirus receptor	Y	N	
EOS01522	1_M36429	postmeiotic segregation increased 2-like 12	N	N	
EOS32094	1_U84573	procollagen-lysine; 2-oxoglutarate 5-dioxygenase (ly	N	N	
EOS07374	A_W28391	proliferation-associated 2G4; 38kD	N	N	
EOS01086	1_L13977	prolylcarboxypeptidase (angiotensinase C)	Y	N	
EOS34913	1_D28235 1_U0463	prostaglandin-endoperoxide synthase 2 (prostagland	Y	N	
EOS01770	1_M93056	protease inhibitor 2 (anti-elastase); monocyte/neutro	N	Type Ib (Nex	YType Ib (Nexo Ccyt)

Table 2, cont.

EOS01861	1_S76965	Protein kinase inhibitor (human; neuroblastoma cell I	N		N
EOS03401	1_Y00815	protein tyrosine phosphatase; receptor type; F	N		N
EOS34011	1_L77886	protein tyrosine phosphatase; receptor type; K	Y	Type Ib (Nex	YType Ib (Nexo Ccyt)
EOS00138	1_D26129	ribonuclease; RNase A family; 1 (pancreatic)	Y	Type Ib (Nex	YType Ib (Nexo Ccyt)
EOS30425	D_RC_AA243278_I	ribosomal protein; mitochondrial; L12	N		N
EOS29398	1_J03040	secreted protein; acidic; cysteine-rich (osteonectin)	N		N
EOS01415	1_M24736	selectin E (endothelial adhesion molecule 1)	Y	Type Ia	YType Ia
EOS01942	1_U03057	singed (Drosophila)-like (sea urchin fascin homolog I	N		N
EOS00549	1_HG2639-HT2735	Single-Stranded Dna-Binding Protein Mssp-1			
EOS32244	A_AA285290	small EDRK-rich factor 2	N		N
EOS30770	1_Z49269	small inducible cytokine subfamily A (Cys-Cys); me	N		N
EOS28510	1_U82108	solute carrier family 9 (sodium/hydrogen exchanger)	N		N
EOS34168	C_RC_R81509_s	splicing factor; arginine/serine-rich 11	N		N
EOS31249	1_U25997	stanniocalcin	N		N
EOS33150	1_X82200	stimulated trans-acting factor (50 kDa)	N	Type Ib (Nex	YType Ib (Nexo Ccyt)
EOS33384	A_AA090257 D_RC	superoxide dismutase 2; mitochondrial			
EOS03301	1_X91247	thioredoxin reductase 1	N		N
EOS00154	1_D28476	thyroid hormone receptor interactor 12	N		N
EOS33468	1_L14837	tight junction protein 1 (zona occludens 1)	N		N
EOS33905	1_D29992 1_L2762	tissue factor pathway inhibitor 2	Y		N
EOS33006	B_RC_W84341	tissue inhibitor of metalloproteinase 2	N		N
EOS01871	1_M74719	transcription factor 4	N		N
EOS34273	1_D50683	transforming growth factor; beta receptor II (70-80kD	N	Type Ib (Nex	YType Ib (Nexo Ccyt)
EOS01794	1_M95787	transgelin	N		N
EOS01072	1_L12711	transketolase (Wernicke-Korsakoff syndrome)	N		N
EOS31789	1_M90657	transmembrane 4 superfamily member 1	Y	Type IIIa (clv	YType IIIa (clv)
EOS33890	1_M18267 1_Z2472	tropomyosin 1 (alpha)	N		N
EOS33611	1_D78577	tyrosine 3-monooxygenase/tryptophan 5-monooxyg	N		N
EOS03025	1_X60957	tyrosine kinase with immunoglobulin and epidermal	Y		N
EOS33660	1_S73591 D_RC_N	upregulated by 1;25-dihydroxyvitamin D-3	N		N
EOS29118	1_M30257 A_M732	vascular cell adhesion molecule 1	Y	Type IIIa (Nc	YType IIIa (Ncyt Cexo)
EOS31258	1_V01512_ma1	v-fos FBJ murine osteosarcoma viral oncogene hom	N		N
EOS33190	A_AA083572 A_RC	v-ral simian leukemia viral oncogene homolog A (ras	N		N
EOS01330	1_M15990	v-yes-1 Yamaguchi sarcoma viral oncogene homolo	N		N
EOS13125	B_RC_T57112	yc20g11.s1 Stratagene lung (#937210) Homo sapie	N		N

Table 2, cont.

EOS33520	D_RC_T67986_s	yc28e12.s1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:82030 3' similar to			
EOS30587	B_RC_T94452	ye36g7.s1 Stratagene lung (#93721) Homo sapiens	N	N	N
EOS24288	D_RC_N22495	yw35g11.s1 Morton Fetal Cochlea Homo sapiens c	N	N	N
EOS01767	1_M92843	zinc finger protein homologous to Zfp-36 in mouse	N	N	N
EOS26329	N_312729_1	zl16d08.r1 Soares_pregnant_uterus_NbHPU Homo	N	N	N
EOS33680	1_X95735 D_RC_H	zyxin	Y	N	N
EOS29695	M86933	amelogenin (Y chromosome)	Y	N	N
EOS27689	AI369384	arylsulfatase D	N	N	N
EOS31416	X83107	BMX non-receptor tyrosine kinase	N	N	N
EOS32863	AA598702	bone morphogenetic protein 6	N	Y	Type II (Ncyt YType II (Ncyt Cexo)
EOS03210	X79981	cadherin 5; VE-cadherin (vascular epithelium)	Y	Y	Type IIIb (Ne YType IIIb (Nexo Ccyt)
EOS01275	L76380	calcitonin receptor-like	Y	Y	Type IIIa (clv YType IIIa (clv)
EOS33843	W84712	calumenin	Y	N	N
EOS03484	Z18951	caveolin 1; caveolae protein; 22kD	N	Y	Type II (Ncyt YType II (Ncyt Cexo)
EOS01027	L06797	chemokine (C-X-C motif); receptor 4 (fusin)	N	Y	Type IIIb (Ne YType IIIb (Nexo Ccyt)
EOS35279	D83174	collagen-binding protein 2 (colligen 2)	Y	Y	Type Ia YType Ia
EOS01768	M92934	connective tissue growth factor	N	Y	Type Ib (Nex YType Ib (Nexo Ccyt)
EOS00411	HG1098-HT1098	Cystatin D			N
EOS02094	U18300	damage-specific DNA binding protein 2 (48kD)	N	N	Type II (Ncyt YType II (Ncyt Cexo)
EOS01954	U03877	EGF-containing fibulin-like extracellular matrix protei	N	Y	Type II (Ncyt YType II (Ncyt Cexo)
EOS01191	L35545	endothelial cell protein C/activated protein C recepto	N	Y	N
EOS31010	J05008	endothelin 1	Y	N	
EOS17927	N52090	EST			
EOS21265	AA404418	EST			
EOS23893	C13961	EST			N
EOS04395	N24990	ESTs	N	N	N
EOS04694	AA025351	ESTs	N	N	Type II (Ncyt YType II (Ncyt Cexo)
EOS04716	AA027168	ESTs	N	Y	N
EOS04780	AA040465	ESTs	N	N	N
EOS04795	AA045136	ESTs	N	N	N
EOS05108	AA187490	ESTs	N	N	N
EOS05193	AA227926	ESTs	N	N	N
EOS05260	AA234743	ESTs	N	N	Type Ib (Nex YType Ib (Nexo Ccyt)
EOS05659	AA292694	ESTs	N	Y	N
EOS05907	AA406363	ESTs	N	N	

Table 2, cont.

EOS05938	AA411465	ESTs	N	N	N
EOS06054	AA423987	ESTs	N	N	N
EOS06085	AA425309	ESTs	N	N	N
EOS06232	AA435896	ESTs	Y	N	N
EOS06723	AA478778	ESTs	N	N	N
EOS07104	AA621714	ESTs	N	N	N
EOS08686	AA127221	ESTs	N	N	N
EOS08931	AA156125	ESTs	N	N	N
EOS09386	AA232645	ESTs	N	N	N
EOS09698	F10399	ESTs	N	Y	Type II (Ncyt YType II (Ncyt Cexo)
EOS10037	H16772	ESTs	N	N	N
EOS10836	N39584	ESTs	N	N	N
EOS11063	N64436	ESTs	Y	N	N
EOS11690	R26892	ESTs	N	N	N
EOS13003	T33637	ESTs	N	N	N
EOS14991	AA253217	ESTs	N	N	N
EOS15026	AA255991	ESTs			
EOS15075	AA258138	ESTs	N	N	N
EOS15749	AA426573	ESTs	N	Y	Type II (Ncyt YType II (Ncyt Cexo)
EOS15877	AA443793	ESTs	N	N	N
EOS16244	AA490588	ESTs	N	N	N
EOS16519	D59570	ESTs	Y	Y	Type II (Ncyt YType II (Ncyt Cexo)
EOS16663	F13787	ESTs	N	N	N
EOS16953	H88157	ESTs	N	Y	Type II (Ncyt YType II (Ncyt Cexo)
EOS17116	H98988	ESTs	N	N	N
EOS19003	R32894	ESTs	N	N	N
EOS19085	R61715	ESTs			
EOS23453	AA608588	ESTs			
EOS23936	D60302	ESTs	N	N	N
EOS24599	N95477	ESTs	N	N	N
EOS26579	AA856990	ESTs	N	N	N
EOS26802	AA136653	ESTs	N	N	N
EOS27581	AI123976	ESTs	N	N	N
EOS27992	AA379500	ESTs	N	N	N
EOS28922	R49693	ESTs	N	N	N

Table 2, cont.

						N	
						Type II (Ncyt YType II (Ncyt Cexo)	
EOS29244	AA028131	ESTs	N	N		N	
EOS30569	D59711	ESTs	Y	Y		N	
EOS30758	AA053400	ESTs	N	N		N	
EOS31112	AA256153	ESTs	N	N		N	
EOS31503	AA046593	ESTs	N	N		N	
					Type Ib (Nex	YType Ib (Nexo Ccyt)	
EOS31577	AA410480	ESTs	N	Y		N	
EOS31686	D45304	ESTs	N	N		N	
EOS31980	AA136353	ESTs	N	N		N	
EOS32924	AA505133	ESTs	N	N		N	
EOS33091	AA253193	ESTs	Y	N		N	
EOS33130	AA432248	ESTs	N	N		N	
EOS33293	AA479713	ESTs	N	N		N	
EOS34229	AA487558	ESTs	N	N		N	
EOS34981	C15324	ESTs					
EOS35003	AA452000	ESTs	N	N		N	
EOS14451	AA046808	ESTs; Highly similar to 40S RIBOSOMAL PROTEIN	N	N		N	
EOS25285	R45630	ESTs; Highly similar to KIAA0372 [H.sapiens]	N	N		N	
EOS27332	AA358869	ESTs; Highly similar to SEC13-RELATED PROTEIN	N	N		N	
EOS19796	W80814	ESTs; Moderately similar to !!!! ALU SUBFAMILY S	N	N		N	
EOS04882	AA071089	ESTs; Moderately similar to !!!! ALU SUBFAMILY S	Y	N		N	
EOS23463	AA608751	ESTs; Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]					
EOS23090	AA488687	ESTs; Moderately similar to !!!! ALU SUBFAMILY S	Y	N		N	
EOS23403	AA599143	ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]					
EOS05756	AA398243	ESTs; Moderately similar to (defline not available 36	N	N		N	
EOS08776	AA132983	ESTs; Moderately similar to C-1-TETRAHYDROFOL	N	N		N	
EOS25520	R23858	ESTs; Moderately similar to envelope protein [H.sap	Y	N		N	
EOS13853	W80763	ESTs; Moderately similar to FK506-binding protein 65kD [M.musculus]					
EOS21311	AA405747	ESTs; Moderately similar to HMG-box transcription f	N	N		N	
EOS32690	H99198	ESTs; Moderately similar to THYMOSIN BETA-4 [H.	N	N		N	
EOS24805	R70506	ESTs; Moderately similar to transformation-related p	N	N		N	
EOS34919	AA236324	ESTs; Weakly similar to !!!! ALU CLASS A WARNIN	Y	N		N	
EOS18405	N66845	ESTs; Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]					
EOS24777	R60044	ESTs; Weakly similar to !!!! ALU SUBFAMILY J WA	N	N		N	
EOS32606	AA283035	ESTs; Weakly similar to !!!! ALU SUBFAMILY J WA	Y	N		N	
EOS08818	AA135606	ESTs; Weakly similar to !!!! ALU SUBFAMILY SB WARNING ENTRY !!!! [H.sapiens]					

Table 2, cont.

EOS16259	AA496257	ESTs; Weakly similar to (defline not available 35133	N			N	
EOS26441	AI024874	ESTs; Weakly similar to (defline not available 38822	N			N	
EOS16360	AA609717	ESTs; Weakly similar to MICROTUBULE-ASSOCIA	N			N	
EOS05306	AA236559	ESTs; Weakly similar to neuronal thread protein AD	Y	Type II (Ncyt	YType II (Ncyt Cexo)	N	
EOS25033	T95333	ESTs; Weakly similar to Strabismus (D.melanogaste	N	Y		N	
EOS01787	M94856	fatty acid binding protein 5 (psoriasis-associated)	N	N		N	
EOS33537	M34539	FK506-binding protein 1A (12kD)	N	N		N	
EOS33447	X52947	gap junction protein; alpha 1; 43kD (connexin 43)	N	Y	Type IIIa (Nc	YType IIIa (Ncyt Cexo)	
EOS33557	U09587	glycyl-tRNA synthetase	Y	N		N	
EOS02213	U31384	guanine nucleotide binding protein 11	N	N		N	
EOS00414	HG1103-HT1103	Guanine Nucleotide-Binding Protein Rai, Ras-Oncogene Related					
EOS04904	AA085918	H.sapiens HUNK1 mRNA	N	N		N	
EOS03115	X69910	H.sapiens p53 mRNA for transmembrane protein	N	N		N	
EOS32288	X60486	H4 histone family; member G	N	N		N	
EOS03088	X67235	hematopoietically expressed homeobox	Y	N		N	
EOS10936	N53375	Homer; neuronal immediate early gene; 3	N	N		N	
EOS33421	L40395	Homo sapiens clone 23689 mRNA; complete cds	N	N		N	
EOS28976	AA195678	Homo sapiens mRNA for KIAA0465 protein; partial c	N	N		N	
EOS32898	N77151	Homo sapiens mRNA for KIAA0799 protein; partial c	N	N		N	
EOS06353	AA448238	Homo sapiens mRNA for KIAA0915 protein; complet	N	N		N	
EOS00335	D86425	Homo sapiens mRNA for nidogen-2	Y	N		N	
EOS10948	N54067	Homo sapiens mRNA for NIK; partial cds					
EOS30902	AA370302	Homo sapiens mRNA; cDNA DKFZp586I1518 (from	Y	N		N	
EOS04522	R81003	Homo sapiens serine protease mRNA; complete cds	Y	N		N	
EOS01377	M21305	Human alpha satellite and satellite 3 junction DNA sequence					
EOS01098	L15388	Human G protein-coupled receptor kinase (GRK5)	N	N		N	
EOS33621	M85289	Human heparan sulfate proteoglycan (HSPG2) mRN	Y	N		N	
EOS07146	D51069	Human isolate JuSo MUC18 glycoprotein mRNA (3' variant); complete cds					
EOS34018	D43636	Human mRNA for KIAA0096 gene; partial cds	N	N		N	
EOS00350	D86983	Human mRNA for KIAA0230 gene; partial cds	Y	N		N	
EOS32617	AB002301	Human mRNA for KIAA0303 gene; partial cds	N	N		N	
EOS02817	X04729	Human mRNA for plasminogen activator inhibitor typ	N	N		N	
EOS34346	M28882	Human MUC18 glycoprotein mRNA, complete cds	Y	Y	Type Ia	YType Ia	
EOS01644	M68874	Human phosphatidylcholine 2-acylhydrolase (cPLA2	N	N		N	
EOS02171	U27109	Human prepromultimerin mRNA; complete cds	Y	N		N	

Table 2, cont.

EOS29301	M10321	Human von Willebrand factor mRNA, 3' end	Y	N		N	
EOS00648	HG3342-HT3519	Id1					
EOS34091	U97188	IGF-II mRNA-binding protein 3	N	N		N	
EOS02828	X06256	integrin; alpha 5 (fibronectin receptor; alpha polypep	N	N		N	
EOS01490	M32334	intercellular adhesion molecule 2	Y	Y	Type Ia	YType Ia	
EOS33077	D12763	interleukin 1 receptor-like 1	Y	N		N	
EOS02593	U70322	karyopherin (importin) beta 2	N	N		N	
EOS32386	AA114250	KIAA0512 gene product	Y	N		N	
EOS02689	U81607	kinase scaffold protein gravin	N	N		N	
EOS33969	S78569	laminin; alpha 4	Y	N		N	
EOS01604	M61916	laminin; beta 1	Y	N		N	
EOS32420	F13782	LIM binding domain 2	N	N		N	
EOS29814	AA286710	lymphocyte adaptor protein	N	N		N	
EOS02734	U89942	lysyl oxidase-like 2	Y	N		N	
EOS02494	U59423	MAD (mothers against decapentaplegic; Drosophila)	N	N		N	
EOS32666	U68019	MAD (mothers against decapentaplegic; Drosophila)	N	N		N	
EOS02966	X54925	matrix metalloproteinase 1 (interstitial collagenase)	Y	N		N	
EOS02845	X07820	matrix metalloproteinase 10 (stromelysin 2)	Y	N		N	
EOS32343	AA132969	metalloprotease 1 (pitrilysin family)	N	N		N	
EOS33626	D10522	myristoylated alanine-rich protein kinase C substrate	N	N		N	
EOS31067	U85193	nuclear factor I/B	N	N		N	
EOS01473	M31166	pentaxin-related gene; rapidly induced by IL-1 beta	Y	N		N	
EOS01124	L20971	phosphodiesterase 4B; cAMP-specific (dunce (Dros	N	Y	Type Ib (Nex	YType Ib (Nexo Ccyt)	
EOS04824	AA054087	phospholipase A2; group IVC (cytosolic; calcium-ind	N	Y	Type Ib (Nex	YType Ib (Nexo Ccyt)	
EOS32013	Y07867	pirin	N	N		N	
EOS02987	X54936	placental growth factor; vascular endothelial growth f	Y	N		N	
EOS00921	J03764	plasminogen activator inhibitor; type I	N	N		N	
EOS01480	M31551	plasminogen activator inhibitor; type II (arginine-serp	N	N		N	
EOS33915	L34657	platelet/endothelial cell adhesion molecule (CD31 an	Y	Y	Type Ia	YType Ia	
EOS07315	U97519	podocalyxin-like	N	Y	Type IIIa (Nc	YType IIIa (Ncyt Cexo)	
EOS05961	AA412284	poliovirus receptor	Y	N		N	
EOS32094	U84573	procollagen-lysine; 2-oxoglutarate 5-dioxygenase (ly	N	N		N	
EOS03096	X67951	proliferation-associated gene A (natural killer-enhan	N	N		N	
EOS32991	AB000584	prostate differentiation factor	Y	N		N	
EOS02233	U33053	protein kinase C-like 1	N	N		N	

Table 2, cont.

EOS09096	AA179845	RAB6 interacting; kinesin-like (rabkinesin6)	N	N		N	
EOS30425	AA243278	ribosomal protein; mitochondrial; L12	N	N		N	
EOS33544	D67029	SEC14 (S. cerevisiae)-like	N	N		N	
EOS29398	J03040	secreted protein; acidic; cysteine-rich (osteonectin)	Y	N		N	
EOS01415	M24736	selectin E (endothelial adhesion molecule 1)	Y	Y	Type Ia	YType Ia	
EOS01942	U03057	singed (Drosophila)-like (sea urchin fascin homolog l	N	N		N	
EOS32648	AA056731	Sjogren syndrome antigen A2 (60kD; ribonucleoprot	N	N		N	
EOS18509	N68905	small inducible cytokine A5 (RANTES)					
EOS19346	T97188	small inducible cytokine A5 (RANTES)					
EOS34383	X70683	SRY (sex determining region Y)-box 4	N	N		N	
EOS02708	U83463	syndecan binding protein (syntenin)	N	N		N	
EOS34586	X14787	thrombospondin 1	Y	N		N	
EOS33905	D29992	tissue factor pathway inhibitor 2	Y	N		N	
EOS01671	M74719	transcription factor 4	N	N		N	
EOS24589	N93521	transcription factor 4	N	N		N	
EOS31789	M90657	transmembrane 4 superfamily member 1	Y	Y	Type IIIa (clv	YType IIIa (clv)	
EOS29735	AA012933	tubulin-specific chaperone d	N	N		N	
EOS03025	X60957	tyrosine kinase with immunoglobulin and epidermal	Y	N		N	
EOS26493	W26247	U5 snRNP-specific protein (220 kD); ortholog of S. c	N	N		N	
EOS07225	T34527	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N	Y	N		N	
EOS10914	N52006	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N	N	N		N	
EOS17493	N34287	unc5 (C.elegans homolog) C	Y	Y	Type Ia	YType Ia	
EOS31811	AA010163	upstream regulatory element binding protein 1	N	N		N	
EOS29118	M30257	vascular cell adhesion molecule 1	Y	Y	Type IIIa (Nc	YType IIIa (Ncyt Cexo)	
EOS33480	W80846	vesicle-associated membrane protein 5 (myobrevin)	N	Y	Type II (Ncyt	YType II (Ncyt Cexo)	
EOS24245	H94892	v-ral simian leukemia viral oncogene homolog A (ras	N	N		N	
EOS33190	AA083572	v-ral simian leukemia viral oncogene homolog A (ras	N	N		N	
EOS13125	T57112	yc20g11.s1 Stratagene lung (#937210) Homo sapie	N	N		N	
EOS25020	T91518	ye20f05.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:118305 3' similar t					
EOS30587	T94452	ye36g7.s1 Stratagene lung (#93721) Homo sapiens	N	N		N	
EOS25495	R20839	yg05c07.r1 Soares infant brain 1NIB Homo sapiens	N	N		N	
EOS19104	R71234	yi54c08.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:143054 3' similar to g					
EOS19151	R98105	yr30g11.s1 Soares fetal liver spleen 1NFLS Homo s	N	N		N	
EOS03780	AA187101	zp61b6.r1 Stratagene endothelial cell 937223 Homo	N	N		N	

TABLE 3

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
D86425	Homo sapiens mRNA for nidogen-2	Hs.82733
D86983	Human mRNA for KIAA0230 gene; partial cds	Hs.118893
HG1098-HT1098	Cystatin D	
HG1103-HT1103	"Guanine Nucleotide-Binding Protein Ral, Ras-Oncogene	
HG3342-HT3519	Id1	
J03764	plasminogen activator inhibitor; type I	Hs.82085
L06797	chemokine (C-X-C motif); receptor 4 (fusin)	Hs.89414
L15388	"Human G protein-coupled receptor kinase (GRK5) mRNA,	Hs.211569
L20971	phosphodiesterase 4B; cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E4)	Hs.188
L35545	endothelial cell protein C/activated protein C receptor	Hs.82353
L76380	calcitonin receptor-like	Hs.152175
M21305	Human alpha satellite and satellite 3 junction DNA sequence	Hs.247946
M24736	selectin E (endothelial adhesion molecule 1)	Hs.89546
M31166	pentaxin-related gene; rapidly induced by IL-1 beta	Hs.2050
M31551	plasminogen activator inhibitor; type II (arginine-serpin)	Hs.75716
M32334	intercellular adhesion molecule 2	Hs.83733
M61916	laminin; beta 1	Hs.82124
M68874	"Human phosphatidylcholine 2-acylhydrolase (cPLA2) mRNA,	
M74719	transcription factor 4	Hs.75356
M92934	connective tissue growth factor	Hs.75511
M94856	fatty acid binding protein 5 (psoriasis-associated)	Hs.153179
U03057	singed (Drosophila)-like (sea urchin fascin homolog like)	Hs.118400
U03877	EGF-containing fibulin-like extracellular matrix protein 1	Hs.76224
U18300	damage-specific DNA binding protein 2 (48kD)	Hs.77602
U27109	Human prepromultimerin mRNA; complete cds	Hs.32934
U31384	guanine nucleotide binding protein 11	Hs.83381
U33053	protein kinase C-like 1	Hs.2499
U59423	MAD (mothers against decapentaplegic; Drosophila) homolog 1	Hs.79067
U70322	karyopherin (importin) beta 2	Hs.168075
U81607	kinase scaffold protein gravin	Hs.788
U83463	syndecan binding protein (syntenin)	Hs.8180
U89942	lysyl oxidase-like 2	Hs.83354
X04729	Human mRNA for plasminogen activator inhibitor type 1	
X06256	integrin; alpha 5 (fibronectin receptor; alpha polypeptide)	Hs.149609
X07820	matrix metalloproteinase 10 (stromelysin 2)	Hs.2258
X54925	matrix metalloproteinase 1 (interstitial collagenase)	Hs.83169
X54936	placental growth factor; vascular endothelial growth factor-related	Hs.2894
X60957	tyrosine kinase with immunoglobulin and epidermal growth factor	Hs.78824
X67235	hematopoietically expressed homeobox	Hs.118651

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
X67951	proliferation-associated gene A (natural killer-enhancing factor A)	Hs.180909
X69910	H.sapiens p63 mRNA for transmembrane protein	Hs.74368
X79981	cadherin 5; VE-cadherin (vascular epithelium)	Hs.76206
Z18951	caveolin 1; caveolae protein; 22kD	Hs.247266
AA187101	"zp61b6.r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:624659 5', mRNA sequence"	
N24990	ESTs	Hs.26418
R81003	Homo sapiens serine protease mRNA; complete cds	Hs.154737
AA025351	ESTs	Hs.134797
AA027168	ESTs	Hs.10031
AA040465	ESTs	Hs.8728
AA045136	ESTs	Hs.22575
AA054087	phospholipase A2; group IVC (cytosolic; calcium-independent)	Hs.18858
AA071089	ESTs; Moderately similar to !!!! ALU SUBFAMILY SC WARNING	Hs.187932
AA085918	H.sapiens HUNKI mRNA	Hs.247482
AA187490	ESTs	Hs.21941
AA227926	ESTs	Hs.6682
AA234743	ESTs	Hs.22120
AA236559	ESTs; Weakly similar to neuronal thread protein AD7c-NTP	Hs.8768
AA292694	ESTs	Hs.3807
AA398243	ESTs; Moderately similar to (define not available 3694664)	Hs.21806
AA406363	ESTs	Hs.30822
AA411465	ESTs	Hs.8619
AA412284	poliovirus receptor	Hs.171844
AA423987	ESTs	Hs.7567
AA425309	ESTs	Hs.33287
AA435896	ESTs	Hs.18397
AA448238	Homo sapiens mRNA for KIAA0915 protein; complete cds	Hs.16714
AA478778	ESTs	Hs.16450
AA621714	ESTs	Hs.25338
D51069	Human isolate JuSo MUC18 glycoprotein mRNA (3' variant);	Hs.211579
T34527	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1)	Hs.80120
U97519	podocalyxin-like	Hs.16426
AA127221	ESTs	Hs.71059
AA132983	ESTs; Moderately similar to C-1-TETRAHYDROFOLATE SYNTHASE; CYTOPLASMIC [H.sapiens]	Hs.44155
AA135606	ESTs; Weakly similar to !!!! ALU SUBFAMILY SB WARNING	Hs.189384
AA156125	ESTs	Hs.72116
AA179845	RAB6 interacting; kinesin-like (rabkinesin6)	Hs.73625
AA232645	ESTs	Hs.42699
F10399	ESTs	Hs.14763

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
H16772	ESTs	Hs.31444
N39584	ESTs	Hs.17404
N52006	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1)	Hs.80120
N53375	Homer; neuronal immediate early gene; 3	Hs.166146
N54067	Homo sapiens mRNA for NIK; partial cds	Hs.3628
N64436	ESTs	Hs.20813
R26892	ESTs	Hs.221434
T33637	ESTs	Hs.6841
T57112	"yc20g11.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:81284 3', mRNA sequence."	
W80763	ESTs; Moderately similar to FK506-binding protein 65kD	Hs.3849
AA046808	ESTs; Highly similar to 40S RIBOSOMAL PROTEIN S27	Hs.108957
AA253217	ESTs	Hs.41271
AA255991	ESTs	Hs.175319
AA258138	ESTs	Hs.88297
AA426573	ESTs	Hs.41135
AA443793	ESTs	Hs.94761
AA490588	ESTs	Hs.43118
AA496257	ESTs; Weakly similar to (defline not available 3513303)	Hs.72165
AA609717	ESTs; Weakly similar to MICROTUBULE-ASSOCIATED	Hs.66048
D59570	ESTs	Hs.17132
F13787	ESTs	Hs.58596
H88157	ESTs	Hs.41105
H98988	ESTs	Hs.42612
N34287	unc5 (C.elegans homolog) C	Hs.44553
N52090	EST	Hs.47420
N66845	ESTs; Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!!	Hs.165411
N68905	small inducible cytokine A5 (RANTES)	
R32894	ESTs	Hs.45514
R61715	ESTs	Hs.138237
R71234	"yi54c08.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:143054 3' similar to gb|M87908|HUMALNE32 Human carcinoma cell-derived Alu RNA transcript, (rRNA); gb:S41458 ROD CGMP-SPECIFIC 3',5'-CYCLIC PHOSPHODIESTERASE	
R98105	"yr30g11.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:206852 3', mRNA sequence."	
T97186	small inducible cytokine A5 (RANTES)	
W80814	ESTs; Moderately similar to !!!! ALU SUBFAMILY SB WARNING	Hs.193700
AA404418	EST	Hs.144953
AA405747	ESTs; Moderately similar to HMG-box transcription factor	Hs.97865

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
AA488687	ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WARNING	Hs.190307
AA599143	ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WARNING	
AA608588	ESTs	Hs.193634
AA608751	ESTs; Moderately similar to !!!! ALU SUBFAMILY SC WARNING	Hs.244904
C13961	EST	Hs.210115
D60302	ESTs	Hs.108977
H94892	v-ral simian leukemia viral oncogene homolog A (ras related)	Hs.6906
N93521	transcription factor 4	Hs.241362
N95477	ESTs	Hs.102943
R60044	ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING	Hs.106706
R70506	ESTs; Moderately similar to transformation-related protein	Hs.107159
T91518	"ye20f05.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:118305 3' similar to contains Alu repetitive element;contains MER12 repetitive element ;, mRNA sequence."	
T95333	ESTs; Weakly similar to Strabismus [D.melanogaster]	Hs.122730
R45630	ESTs; Highly similar to KIAA0372 [H.sapiens]	Hs.170098
R20839	"yg05c07.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:31444 5', mRNA sequence."	
R23858	ESTs; Moderately similar to envelope protein [H.sapiens]	Hs.23986
AI024874	ESTs; Weakly similar to (defline not available 3882257)	Hs.57958
W26247	U5 snRNP-specific protein (220 kD); ortholog of S. cerevisiae	Hs.6413
AA856990	ESTs	Hs.125058
AA136653	ESTs	
AA358869	ESTs; Highly similar to SEC13-RELATED PROTEIN [H.sapiens]	Hs.227949
AI123976	ESTs	Hs.105689
AI369384	arylsulfatase D	
AA379500	ESTs	Hs.193155
R49693	ESTs	Hs.107708
AA195678	Homo sapiens mRNA for KIAA0465 protein; partial cds	Hs.108258
M30257	vascular cell adhesion molecule 1	Hs.109225
AA028131	ESTs	Hs.110342
M10321	"Human von Willebrand factor mRNA, 3' end"	Hs.110802
J03040	secreted protein; acidic; cysteine-rich (osteonectin)	Hs.111779
M86933	amelogenin (Y chromosome)	Hs.1238
AA012933	tubulin-specific chaperone d	Hs.241687
AA286710	lymphocyte adaptor protein	Hs.13131
AA243278	ribosomal protein; mitochondrial; L12	Hs.109059
D59711	ESTs	Hs.237289
T94452	"ye36g7.s1 Stratagene lung (#93721) Homo sapiens cDNA clone IMAGE:119868 3', mRNA sequence"	Hs.241207

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
AA053400	ESTs	Hs.241227
AA370302	Homo sapiens mRNA; cDNA DKFZp586I1518 (from clone	Hs.21739
J05008	endothelin 1	Hs.2271
U85193	nuclear factor I/B	Hs.33287
AA256153	ESTs	Hs.23912
X83107	BMX non-receptor tyrosine kinase	Hs.27372
AA046593	ESTs	Hs.28959
AA410480	ESTs	Hs.30089
D45304	ESTs	Hs.31595
M90657	transmembrane 4 superfamily member 1	Hs.3337
AA010163	upstream regulatory element binding protein 1	Hs.3383
AA136353	ESTs	Hs.38022
Y07867	pirin	Hs.38842
U84573	procollagen-lysine; 2-oxoglutarate 5-dioxygenase (lysine	Hs.41270
X60486	H4 histone family; member G	Hs.46423
AA132969	metalloprotease 1 (pitrilysin family)	Hs.4812
AA114250	KIAA0512 gene product	Hs.48924
F13782	LIM binding domain 2	Hs.4980
AA283035	ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING	Hs.54813
AB002301	Human mRNA for KIAA0303 gene; partial cds	Hs.54985
AA056731	Sjogren syndrome antigen A2 (60kD; ribonucleoprotein	Hs.554
U68019	MAD (mothers against decapentaplegic; Drosophila) homolog 3	Hs.211578
H99198	ESTs; Moderately similar to THYMOSIN BETA-4 [H.sapiens]	Hs.56145
AA598702	bone morphogenetic protein 6	Hs.6101
N77151	Homo sapiens mRNA for KIAA0799 protein; partial cds	Hs.61638
AA505133	ESTs	Hs.62273
AB000584	prostate differentiation factor	Hs.116577
D12763	interleukin 1 receptor-like 1	Hs.66
AA253193	ESTs	Hs.6631
AA432248	ESTs	Hs.6738
AA083572	v-ral simian leukemia viral oncogene homolog A (ras related)	Hs.6906
AA479713	ESTs	Hs.71962
L40395	Homo sapiens clone 23689 mRNA; complete cds	Hs.170001
X52947	gap junction protein; alpha 1; 43kD (connexin 43)	Hs.74471
W80846	vesicle-associated membrane protein 5 (myobrevin)	Hs.74669
M34539	FK506-binding protein 1A (12kD)	Hs.752
D67029	SEC14 (S. cerevisiae)-like	Hs.75232
U09587	glycyl-tRNA synthetase	Hs.75280
M85289	"Human heparan sulfate proteoglycan (HSPG2) mRNA, complete	Hs.211573
D10522	myristoylated alanine-rich protein kinase C substrate (MARCKS;	Hs.75607
W84712	calumenin	Hs.7753
D29992	tissue factor pathway inhibitor 2	Hs.78045

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
L34657	platelet/endothelial cell adhesion molecule (CD31 antigen)	Hs.78146
S78569	laminin; alpha 4	Hs.78672
D43636	Human mRNA for KIAA0096 gene; partial cds	Hs.79025
U97188	IGF-II mRNA-binding protein 3	Hs.79440
AA487558	ESTs	Hs.8135
M28882	"Human MUC18 glycoprotein mRNA, complete cds"	Hs.211579
X70683	SRY (sex determining region Y)-box 4	Hs.83484
X14787	thrombospondin 1	Hs.87409
AA236324	ESTs; Weakly similar to !!!! ALU CLASS A WARNING ENTRY !!!!	Hs.92381
C15324	ESTs	Hs.93668
AA452000	ESTs	Hs.94030
D83174	collagen-binding protein 2 (colligen 2)	Hs.9930
D00596	Homo sapiens gene for thymidylate synthase; exons 1; 2; 3; 4; 5;	Hs.196351
D11428	peripheral myelin protein 22	Hs.103724
D13640	major histocompatibility complex; class I; C	Hs.183618
D14874	adrenomedullin	Hs.394
D26129	ribonuclease; RNase A family; 1 (pancreatic)	Hs.78224
D28476	thyroid hormone receptor interactor 12	Hs.138617
D86425	Homo sapiens mRNA for nidogen-2	Hs.82733
D86983	Human mRNA for KIAA0230 gene; partial cds	Hs.118893
D87953	N-myc downstream regulated	Hs.75789
HG1862-HT1897	Calmodulin Type I	
HG2614-HT2710	"Collagen, Type Viii, Alpha 1"	
HG2639-HT2735	Single-Stranded Dna-Binding Protein Mssp-1	
HG2855-HT2995	"Heat Shock Protein, 70 Kda (Gb:Y00371)"	
HG3044-HT3742	"Fibronectin, Alt. Splice 1"	
HG3342-HT3519	Id1	
HG3543-HT3739	Insulin-Like Growth Factor 2	
HG4069-HT4339	Monocyte Chemotactic Protein 1	
HG417-HT417	Cathepsin B	
J03764	plasminogen activator inhibitor; type I	Hs.82085
L06797	chemokine (C-X-C motif); receptor 4 (fusin)	Hs.89414
L08246	myeloid cell leukemia sequence 1 (BCL2-related)	Hs.86386
L12711	transketolase (Wernicke-Korsakoff syndrome)	Hs.89643
L13977	prolylcarboxypeptidase (angiotensinase C)	Hs.75693
L15388	"Human G protein-coupled receptor kinase (GRK5) mRNA,	
L19871	activating transcription factor 3	Hs.460
L20859	Human leukemia virus receptor 1 (GLVR1) mRNA; complete cds	Hs.78452
L42176	four and a half LIM domains 2	Hs.8302
L49169	Human G0S3 mRNA; complete cds	Hs.75678
L76380	calcitonin receptor-like	Hs.152175
M15990	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1	Hs.194148
M23254	calpain; large polypeptide L2	Hs.76288

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
M24736	selectin E (endothelial adhesion molecule 1)	Hs.89546
M26576	collagen; type IV; alpha 1	Hs.119129
M27396	asparagine synthetase	Hs.75692
M31166	pentaxin-related gene; rapidly induced by IL-1 beta	Hs.2050
M31994	"Homo sapiens aldehyde dehydrogenase (ALDH1) gene, exon 13	
M32334	intercellular adhesion molecule 2	Hs.83733
M35878	insulin-like growth factor binding protein 3	Hs.77326
M36429	postmeiotic segregation increased 2-like 12	Hs.89672
M57730	ephrin-A1	Hs.1624
M57731	GRO2 oncogene	Hs.75765
M60858	nucleolin	Hs.79110
M62994	filamin B; beta (actin-binding protein-278)	Hs.81008
M68874	"Human phosphatidylcholine 2-acylhydrolase (cPLA2) mRNA,	
M69043	nuclear factor of kappa light polypeptide gene enhancer in B-cells	Hs.81328
M74719	transcription factor 4	Hs.75356
M75126	hexokinase 1	Hs.118625
M84349	CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5; EJ16; EJ30; EL32 and G344)	Hs.119663
M92843	zinc finger protein homologous to Zfp-36 in mouse	Hs.198309
M92934	connective tissue growth factor	Hs.75511
M93056	protease inhibitor 2 (anti-elastase); monocyte/neutrophil	Hs.183583
M94856	fatty acid binding protein 5 (psoriasis-associated)	Hs.153179
M95787	transgelin	Hs.75777
S76965	Protein kinase inhibitor [human; neuroblastoma cell line	Hs.75209
S81914	DIFFERENTIATION-DEPENDENT GENE 2	Hs.76095
U03057	singed (Drosophila)-like (sea urchin fascin homolog like)	Hs.118400
U03100	catenin (cadherin-associated protein); alpha 1 (102kD)	Hs.178452
U03877	EGF-containing fibulin-like extracellular matrix protein 1	Hs.76224
U08021	nicotinamide N-methyltransferase	Hs.76669
U14391	myosin IC	Hs.82251
U31384	guanine nucleotide binding protein 11	Hs.83381
U32944	dynein; cytoplasmic; light polypeptide	Hs.5120
U40369	"Human spermidine/spermine N1-acetyltransferase (SSAT) gene,	
U41767	"Human metargidin precursor mRNA, complete cds"	
U48959	Homo sapiens myosin light chain kinase (MLCK) mRNA;	Hs.75950
U51010	"Human nicotinamide N-methyltransferase gene, exon 1 and 5'	
U51478	ATPase; Na+/K+ transporting; beta 3 polypeptide	Hs.76941
U53445	Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA; complete cds	Hs.15432
U59289	cadherin 13; H-cadherin (heart)	Hs.63984
U59423	MAD (mothers against decapentaplegic; Drosophila) homolog 1	Hs.79067
U62015	"Homo sapiens Cyr61 mRNA, complete cds"	

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
U63825	Human hepatitis delta antigen interacting protein A (dipA) mRNA;	Hs.66713
U67963	Human lysophospholipase homolog (HU-K5) mRNA; complete	Hs.6721
U73379	Human cyclin-selective ubiquitin carrier protein mRNA; complete	Hs.93002
U73824	eukaryotic translation initiation factor 4 gamma; 2	Hs.183684
U77604	microsomal glutathione S-transferase 2	Hs.81874
U81607	kinase scaffold protein gravin	Hs.788
U89942	lysyl oxidase-like 2	Hs.83354
X04412	gelsolin (amyloidosis; Finnish type)	Hs.80562
X06985	heme oxygenase (decycling) 1	Hs.75967
X07820	matrix metalloproteinase 10 (stromelysin 2)	Hs.2258
X12876	keratin 18	Hs.65114
X15729	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 5 (RNA helicase;	Hs.76053
X52541	early growth response 1	Hs.738
X53416	filamin A; alpha (actin-binding protein-280)	Hs.76279
X54489	GRO1 oncogene (melanoma growth stimulating activity; alpha)	Hs.789
X54925	matrix metalloproteinase 1 (interstitial collagenase)	Hs.83169
X57206	inositol 1;4;5-trisphosphate 3-kinase B	Hs.78877
X59798	cyclin D1 (PRAD1: parathyroid adenomatosis 1)	Hs.82932
X60957	tyrosine kinase with immunoglobulin and epidermal growth factor	Hs.78824
X65965	H.sapiens SOD-2 gene for manganese superoxide dismutase	
X69111	inhibitor of DNA binding 3; dominant negative helix-loop-helix	Hs.76884
X70940	eukaryotic translation elongation factor 1 alpha 2	Hs.2642
X87838	catenin (cadherin-associated protein); beta 1 (88kD)	Hs.171271
X91247	thioredoxin reductase 1	Hs.13046
X97748	H.sapiens PTX3 gene promotor region	
Y00815	protein tyrosine phosphatase; receptor type; F	Hs.75216
AA303711	ephrin-B1	Hs.144700
L44538	ESTs	Hs.156044
AA025351	ESTs	Hs.134797
AA027050	ESTs	Hs.31189
AA029462	ESTs	Hs.17235
AA045136	ESTs	Hs.22575
AA047437	ESTs	Hs.22968
AA054087	phospholipase A2; group IVC (cytosolic; calcium-independent)	Hs.18858
AA071089	ESTs; Moderately similar to !!!! ALU SUBFAMILY SC WARNING	Hs.187932
AA156450	ESTs; Weakly similar to Similar to Rat trg gene product	Hs.8982
AA187490	ESTs	Hs.21941
AA195031	ESTs; Moderately similar to PROBABLE G PROTEIN-COUPLED RECEPTOR APJ [H.sapiens]	Hs.9305
AA205724	ESTs	Hs.10119
AA227926	ESTs	Hs.6682

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
AA227986	ESTs	Hs.25329
AA234743	ESTs	Hs.22120
AA253216	ESTs	Hs.22283
AA256210	oncomodulin	Hs.199134
AA256268	ESTs	Hs.10283
AA279397	ESTs; Moderately similar to fibronectin [H.sapiens]	Hs.25001
AA292379	ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WARNING	Hs.20340
AA292717	ESTs; Weakly similar to JM2 [H.sapiens]	Hs.7891
AA346551	ESTs	Hs.23457
AA400292	ESTs	Hs.23786
AA404338	ESTs	Hs.21812
AA412284	poliovirus receptor	Hs.171844
AA423987	ESTs	Hs.7567
AA428594	ESTs	Hs.21321
AA430108	ESTs	Hs.6019
AA431462	ESTs	Hs.28329
AA431470	ESTs; Weakly similar to CAMP-DEPENDENT PROTEIN KINASE INHIBITOR; MUSCLE/BRAIN FORM [H.sapiens]	Hs.3407
AA443756	ESTs; Moderately similar to (defline not available 4105275)	Hs.6673
AA449479	ESTs; Highly similar to (defline not available 5106787)	Hs.5216
AA459916	bradykinin receptor B2	Hs.25021
AA465226	ESTs	Hs.28631
AA478778	ESTs	Hs.16450
AA479037	ESTs	Hs.7961
AA482597	ESTs; Highly similar to (defline not available 4704739)	Hs.26054
AA487561	ESTs; Highly similar to RAS-RELATED PROTEIN RAB-1A	Hs.9813
AA489245	ESTs; Weakly similar to sperm specific protein [H.sapiens]	Hs.5682
AA504110	ESTs	Hs.18063
AA520989	ESTs; Highly similar to SERINE/THREONINE PROTEIN PHOSPHATASE PP1-BETA CATALYTIC SUBUNIT [H.sapiens]	Hs.9195
AA599434	ESTs	Hs.25035
AA608649	Homo sapiens clone 23742 mRNA; partial cds	Hs.6354
AA609519	ESTs	Hs.26458
D51069	Human isolate JuSo MUC18 glycoprotein mRNA (3' variant);	Hs.185718
U97519	podocalyxin-like	Hs.16426
W28391	proliferation-associated 2G4; 38kD	Hs.5181
AA035638	Homo sapiens mRNA; cDNA DKFZp564F053 (from clone	Hs.71968
AA083514	ESTs	Hs.68301
AA121315	ESTs	Hs.70823
AA147186	ESTs	Hs.92387
AA156125	ESTs	Hs.72116
AA188932	ESTs	Hs.85640

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
AA219653	ESTs	Hs.87125
AA232645	ESTs	Hs.42699
F10078	ESTs	Hs.13233
H48032	ESTs	Hs.9645
H82117	ESTs	Hs.28043
N39584	ESTs	Hs.17404
N54067	Homo sapiens mRNA for NIK; partial cds	Hs.3628
N59858	ESTs	Hs.33032
N90933	ESTs	Hs.4867
N93764	ESTs; Moderately similar to !!!! ALU CLASS C WARNING ENTRY	Hs.10175
R26124	ESTs	Hs.24024
R27957	ESTs	Hs.24230
R55470	ESTs; Moderately similar to K02E10.2 [C.elegans]	Hs.11067
T16550	ESTs; Highly similar to vacuolar protein sorting homolog h-vps45	Hs.6650
T26674	ESTs; Weakly similar to neuronal thread protein AD7c-NTP	Hs.6966
T57112	"yc20g11.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:81284 3', mRNA sequence."	Hs.8881
T88700	ESTs	Hs.173374
T90527	ESTs	Hs.7890
W42789	ESTs	Hs.31446
W60002	plastin 3 (T isoform)	Hs.4114
W78175	ESTs	Hs.17901
W84768	ESTs	Hs.141742
W94427	ESTs; Weakly similar to Na;K-ATPase gamma subunit	Hs.3807
AA253217	ESTs	Hs.41271
AA426573	ESTs	Hs.41135
AA432374	ESTs	Hs.48029
AA446622	ESTs	Hs.74313
AA478771	ESTs	Hs.50841
AA482594	ESTs	Hs.62684
AA490588	ESTs	Hs.43118
D59570	ESTs	Hs.17132
H88157	ESTs	Hs.41105
H94648	ESTs	Hs.41995
H97538	ESTs	Hs.42392
H98670	ESTs; Weakly similar to (defline not available 4884081)	Hs.49753
N22107	ESTs; Moderately similar to !!!! ALU SUBFAMILY SC WARNING	Hs.172241
W38197	Accession not listed in Genbank	
W80814	ESTs; Moderately similar to !!!! ALU SUBFAMILY SB WARNING	Hs.196785
AA287347	ESTs	Hs.105088
AA402799	ESTs	Hs.182538

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
AA404418	EST	Hs.144953
AA425107	ESTs	Hs.97016
AA425435	ESTs; Moderately similar to !!!! ALU SUBFAMILY J WARNING	Hs.98438
AA442872	ESTs	Hs.110771
AA452860	ESTs; Moderately similar to !!!! ALU SUBFAMILY SP WARNING	Hs.197214
AA488687	ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WARNING	Hs.190307
AA599674	ESTs; Weakly similar to ORF [D.melanogaster]	Hs.108115
F13673	ESTs	Hs.99769
H99093	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide (72kD)	Hs.6179
N22495	"yw35g11.s1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:254276 3', mRNA sequence."	Hs.102415
N23031	myosin; heavy polypeptide 7; cardiac muscle; beta	Hs.929
R15740	carbohydrate (chondroitin 6/keratan) sulfotransferase 1	Hs.104576
R39610	calpain; large polypeptide L2	Hs.76288
W45560	ESTs	Hs.102541
Z39833	H.sapiens mRNA for Rho6 protein	Hs.124940
Z40583	ESTs	Hs.101259
AA825437	ESTs	
R66613	Homo sapiens mRNA; cDNA DKFZp564F053 (from clone	
AA868063	carbohydrate (chondroitin 6/keratan) sulfotransferase 1	
AA128075	"zl16d08.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:502095 5', mRNA sequence."	
N66570	ESTs	
AI051390	ESTs	
AA627122	ESTs	
X02761	fibronectin 1	Hs.118162
AF010193	MAD (mothers against decapentaplegic; Drosophila) homolog 7	Hs.100602
AA149044	ESTs; Highly similar to the KIAA0195 gene is expressed	Hs.10086
U82108	solute carrier family 9 (sodium/hydrogen exchanger); isoform 3	Hs.101813
D78676	ESTs; Moderately similar to (defline not available 4529890)	Hs.105509
L35240	enigma (LIM domain protein)	Hs.102948
AA598737	lactate dehydrogenase B	Hs.180414
R69417	ESTs	Hs.107055
AA232837	ESTs; Weakly similar to Human pre-mRNA cleavage factor I 68 kDa subunit [H.sapiens]	Hs.107125
N72695	ESTs	Hs.108557
M30257	vascular cell adhesion molecule 1	Hs.109225
M96843	inhibitor of DNA binding 2; dominant negative helix-loop-helix protein	Hs.109617
X68277	dual specificity phosphatase 1	Hs.171695
AA292440	myeloid differentiation primary response	Hs.110571
J03040	secreted protein; acidic; cysteine-rich (osteonectin)	Hs.111779

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
AA228107	ESTs	Hs.54642
AA449789	connective tissue growth factor	Hs.75511
W01367	ESTs	Hs.170980
AA610116	ESTs; Highly similar to (defline not available 4325180)	Hs.11663
AA258308	Homo sapiens mRNA; cDNA DKFZp564F053 (from clone	Hs.165618
AA460273	Homo sapiens mRNA for KIAA0517 protein; partial cds	Hs.12372
AA286710	lymphocyte adaptor protein	Hs.13131
T68873	metallothionein 1L	Hs.143289
D63476	PAK-interacting exchange factor beta	Hs.172813
M62403	insulin-like growth factor-binding protein 4	Hs.1516
X55740	5' nucleotidase (CD73)	Hs.153952
L10284	calnexin	Hs.155560
AA243278	ribosomal protein; mitochondrial; L12	Hs.109059
AA430032	pituitary tumor-transforming 1	Hs.159626
H16402	ESTs	Hs.17121
D59711	ESTs	Hs.17132
T94452	"ye36g7.s1 Stratagene lung (#93721) Homo sapiens cDNA clone IMAGE:119868 3', mRNA sequence"	
AA431571	ESTs	Hs.17894
R79356	Homo sapiens mRNA for KIAA0544 protein; partial cds	Hs.19280
AA280375	ESTs	Hs.19928
Z49269	small inducible cytokine subfamily A (Cys-Cys); member 14	Hs.20144
Z41740	ESTs	Hs.24462
AA121543	Homo sapiens mRNA for KIAA0758 protein; partial cds	Hs.22039
J05008	endothelin 1	Hs.2271
AA101878	ESTs	Hs.22793
T35341	ESTs; Highly similar to (defline not available 4519883) [H.sapiens]	Hs.22880
N87590	ESTs	Hs.23037
AA256153	ESTs	Hs.23912
W74533	Homo sapiens mRNA for KIAA0786 protein; partial cds	Hs.24212
U25997	stanniocalcin	Hs.25590
V01512	v-fos FBJ murine osteosarcoma viral oncogene homolog	Hs.25647
V01512	v-fos FBJ murine osteosarcoma viral oncogene homolog	Hs.25647
V01512	v-fos FBJ murine osteosarcoma viral oncogene homolog	Hs.25647
V01512	v-fos FBJ murine osteosarcoma viral oncogene homolog	Hs.25647
X56681	jun D proto-oncogene	Hs.2780
AA161292	interferon; alpha-inducible protein 27	Hs.2867
AA491465	ESTs	Hs.28792
AA046593	ESTs	Hs.28959
D50914	Human mRNA for KIAA0124 gene; partial cds	Hs.30736
D45304	ESTs	Hs.31595
M90657	transmembrane 4 superfamily member 1	Hs.3337

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
W69127	ESTs; Weakly similar to zinc finger protein ZNF191 [H.sapiens]	Hs.3449
AA316186	ESTs; Highly similar to (defline not available 4262136)	Hs.34549
AA384503	ESTs	Hs.179260
AA136353	ESTs	Hs.38022
AA044755	ESTs; Weakly similar to !!!! ALU SUBFAMILY SX WARNING	Hs.173705
U84573	procollagen-lysine; 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2	Hs.41270
AA058911	ESTs; Weakly similar to membrane glycoprotein [M.musculus]	Hs.4193
AA620962	dynein; cytoplasmic; light intermediate polypeptide 2	Hs.44251
AA285290	small EDRK-rich factor 2	Hs.44499
X60486	H4 histone family; member G	Hs.46423
R31641	ESTs	Hs.197148
AA489190	ESTs	Hs.48320
F13782	LIM binding domain 2	Hs.4980
AA257993	Janus kinase 1 (a protein tyrosine kinase)	Hs.50651
M24283	intercellular adhesion molecule 1 (CD54); human rhinovirus	Hs.168383
AA443114	ESTs; Weakly similar to PIM-1 PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE [H.sapiens]	Hs.5326
T35289	casein kinase 1; alpha 1	Hs.195206
N23817	Homo sapiens clone 23675 mRNA sequence	Hs.5807
AA047151	ESTs	Hs.5897
N77151	Homo sapiens mRNA for KIAA0799 protein; partial cds	Hs.61638
AA480074	ESTs	Hs.62206
Y00787	interleukin 8	Hs.624
T99789	ESTs	Hs.64313
W84341	tissue inhibitor of metalloproteinase 2	Hs.6441
L09209	amyloid beta (A4) precursor-like protein 2	Hs.64797
D12763	interleukin 1 receptor-like 1	Hs.66
T16484	ESTs	Hs.6607
AA253193	ESTs	Hs.6631
AA432248	ESTs	Hs.6738
X82200	stimulated trans-acting factor (50 kDa)	Hs.68054
AA083572	v-ral simian leukemia viral oncogene homolog A (ras related)	Hs.6906
L00352	low density lipoprotein receptor (familial hypercholesterolemia)	Hs.181182
N75791	ESTs	Hs.7153
X57579	H.sapiens activin beta-A subunit (exon 2)	
X02612	cytochrome P450; subfamily I (aromatic compound-inducible);	Hs.72912
H44631	immediate early protein	Hs.737
AA090257	superoxide dismutase 2; mitochondrial	Hs.177781
X83703	H.sapiens mRNA for cytokine inducible nuclear protein	Hs.74019
L40395	Homo sapiens clone 23689 mRNA; complete cds	Hs.170001
AA227913	ESTs	Hs.198456

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
X52947	gap junction protein; alpha 1; 43kD (connexin 43)	Hs.74471
M11313	alpha-2-macroglobulin	Hs.74561
L14837	tight junction protein 1 (zona occludens 1)	Hs.74614
M60721	"Human homeobox gene, complete cds"	
D90209	activating transcription factor 4 (tax-responsive enhancer element	Hs.181243
T67986	"yc28e12.s1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:82030 3' similar to gb:X14723 CLUSTERIN	Hs.75106
AA148318	Human mRNA for KIAA0069 gene; partial cds	Hs.75249
U97105	dihydropyrimidinase-like 2	Hs.173381
T25747	H.sapiens OZF mRNA	Hs.75471
K02574	Accession not listed in Genbank	
D78577	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein; eta polypeptide	Hs.75544
X53331	matrix Gla protein	Hs.75742
S73591	upregulated by 1;25-dihydroxyvitamin D-3	Hs.179526
X95735	zyxin	Hs.75873
L16862	G protein-coupled receptor kinase 6	Hs.76297
U44975	Homo sapiens Kruppel-like zinc finger protein Zf9 mRNA;	Hs.76526
M97796	inhibitor of DNA binding 2; dominant negative helix-loop-helix	Hs.180919
U86782	26S proteasome-associated pad1 homolog	Hs.178761
AA099391	ESTs	Hs.77310
M19267	tropomyosin 1 (alpha)	Hs.77899
D29992	tissue factor pathway inhibitor 2	Hs.78045
L19314	phosphorylase kinase; beta	Hs.195217
S78569	laminin; alpha 4	Hs.78672
U28811	"Human cysteine-rich fibroblast growth factor receptor (CFR-1)	
L77886	protein tyrosine phosphatase; receptor type; K	Hs.79005
C14407	neuronal tissue-enriched acidic protein	Hs.79516
M60278	diphtheria toxin receptor (heparin-binding epidermal growth	Hs.799
R81509	splicing factor; arginine/serine-rich 11	Hs.184571
AA487558	ESTs	Hs.8135
D86962	KIAA0207 gene product	Hs.81875
AA478971	disabled (Drosophila) homolog 2 (mitogen-responsive	Hs.81988
D50683	transforming growth factor; beta receptor II (70-80kD)	Hs.82028
U56637	capping protein (actin filament) muscle Z-line; alpha 1	Hs.184270
M61199	Human cleavage signal 1 protein mRNA; complete cds	Hs.82767
M28882	"Human MUC18 glycoprotein mRNA, complete cds"	
X15183	CDW52 antigen (CAMPATH-1 antigen)	Hs.180532
S53911	CD34	Hs.85289

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
U20734	Human transcription factor junB (junB) gene; 5' region and	Hs.198951
D28235	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H	Hs.92309
AA236324	ESTs; Weakly similar to !!!! ALU CLASS A WARNING ENTRY !!!!	Hs.92381
AA148923	Homo sapiens mRNA for DEPP (decidual protein induced by	Hs.93675
AA174183	ESTs	Hs.93872
AA456311	ESTs; Weakly similar to !!!! ALU CLASS A WARNING ENTRY !!!!	Hs.93961
L08069	heat shock protein; DNAJ-like 2	Hs.94
AA452000	ESTs	Hs.94030
AA282140	ESTs	Hs.9587
J02854	myosin regulatory light chain 2; smooth muscle isoform	Hs.9615
AA442054	phospholipase C; gamma 1 (formerly subtype 148)	Hs.993
AB000450	vaccinia related kinase 2	
AB002380	KIAA0382 protein	
AB003103	proteasome (prosome; macropain) 26S subunit; non-ATPase; 12	
AB004884	tousled-like kinase 2	
AF000573	homogentisate 1;2-dioxygenase (homogentisate oxidase)	
AF008937		
AF009301	similar to S. cerevisiae SSM4	
AF009368	cAMP responsive element binding protein 3 (luman)	
D00591	chromosome condensation 1	
D00760	proteasome (prosome; macropain) subunit; alpha type; 2	
D11139	tissue inhibitor of metalloproteinase 1 (erythroid potentiating	
D14657	KIAA0101 gene product	
D14878	D123 gene product	
D17716	mannosyl (alpha-1;6-)-glycoprotein beta-1;6-N-acetyl-glucosaminyltransferase	
D21090	RAD23 (S. cerevisiae) homolog B	
D26135	diacylglycerol kinase; gamma (90kD)	
D26528	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 7 (RNA helicase;	
D30742	calcium/calmodulin-dependent protein kinase IV	
D31762	KIAA0057 gene product; TRAM-like protein	
D31765	KIAA0061 protein	
D31888	KIAA0071 protein	
D38128	prostaglandin I2 (prostacyclin) receptor (IP)	
D38500	postmeiotic segregation increased 2-like 4	
D38551	RAD21 (S. pombe) homolog	
D42087	KIAA0118 protein	
D49396	antioxidant protein 1	
D55640		
D63391	platelet-activating factor acetylhydrolase; isoform Ib; gamma	

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
D63477	KIAA0143 protein	
D63483	acetyl LDL receptor; SREC	
D64015	TIA1 cytotoxic granule-associated RNA-binding protein-like 1	
D79990	KIAA0168 gene product	
D79997	KIAA0175 gene product	
D80010	KIAA0188 protein	
D84276	CD38 antigen (p45)	
D86425	nidogen 2	
D86978	KIAA0225 protein	
D87012	Human (lambda) DNA for immunoglobin light chain	
D87075	solute carrier family 23 (nucleobase transporters); member 1	
D87432	solute carrier family 7 (cationic amino acid transporter; y+	
D87448	topoisomerase (DNA) II binding protein	
D87845	platelet-activating factor acetylhydrolase 2 (40kD)	
HG1098-HT1098		
HG2167-HT2237		
HG2415-HT2511		
HG2825-HT2949		
HG2887-HT3031		
HG4660-HT5073		
HG4704-HT5146		
HG884-HT884		
HG919-HT919		
J00212		
J04029	keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et	
J04031	methylenetetrahydrofolate dehydrogenase (NADP+ dependent); methenyltetrahydrofolate cyclohydrolase; formyltetrahydrofolate	
J04088	topoisomerase (DNA) II alpha (170kD)	
J04543	annexin A7	
L06139	TEK tyrosine kinase; endothelial (venous malformations; multiple cutaneous and mucosal)	
L07540	replication factor C (activator 1) 5 (36.5kD)	
L08895	MADS box transcription enhancer factor 2; polypeptide C	
L11239	gastrulation brain homeo box 1	
L11353	neurofibromin 2 (bilateral acoustic neuroma)	
L13773	myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to; 2	
L13800		
L14922	replication factor C (activator 1) 1 (145kD)	
L15189	heat shock 70kD protein 9B (mortalin-2)	
L15388	G protein-coupled receptor kinase 5	
L16895	lysyl oxidase	
L27476	tight junction protein 2 (zona occludens 2)	

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
L27624	tissue factor pathway inhibitor 2	
L32976	mitogen-activated protein kinase kinase kinase 11	
L33404	kallikrein 7 (chymotryptic; stratum corneum)	
L35263	mitogen-activated protein kinase 14	
L37347	solute carrier family 11 (proton-coupled divalent metal ion	
L40371	thyroid hormone receptor interactor 4	
L40391	Homo sapiens (clone s153) mRNA fragment	
L41607	glucosaminyl (N-acetyl) transferase 2; I-branching enzyme	
L77566	DiGeorge syndrome critical region gene DGSI	
M13928	aminolevulinate; delta-; dehydratase	
M13928	aminolevulinate; delta-; dehydratase	
M14016	uroporphyrinogen decarboxylase	
M14219	decorin	
M15796	proliferating cell nuclear antigen	
M21305	Human alpha satellite and satellite 3 junction DNA sequence	
M22092		
M22898	tumor protein p53 (Li-Fraumeni syndrome)	
M22995	RAP1A; member of RAS oncogene family	
M23379	RAS p21 protein activator (GTPase activating protein) 1	
M24364	major histocompatibility complex; class II; DQ beta 1	
M24400	chymotrypsinogen B1	
M25753	cyclin B1	
M27691	cAMP responsive element binding protein 1	
M28213	RAB2; member RAS oncogene family	
M29550	protein phosphatase 3 (formerly 2B); catalytic subunit; alpha	
M29971	O-6-methylguanine-DNA methyltransferase	
M30269	nidogen (enactin)	
M31158	protein kinase; cAMP-dependent; regulatory; type II; beta	
M31166	pentaxin-related gene; rapidly induced by IL-1 beta	
M31210	endothelial differentiation; sphingolipid G-protein-coupled receptor; 1	
M55420	Epsilon ; IgE	
M59979	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H	
M62810	transcription factor 6-like 1 (mitochondrial transcription factor	
M63838	interferon; gamma-inducible protein 16	
M64710	Human CNP gene for C-type natriuretic peptide	
M68874		
M74524	ubiquitin-conjugating enzyme E2A (RAD6 homolog)	
M80254	peptidylprolyl isomerase F (cyclophilin F)	
M81780	sphingomyelin phosphodiesterase 1; acid lysosomal (acid	
M81780	sphingomyelin phosphodiesterase 1; acid lysosomal (acid	

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
M81780	sphingomyelin phosphodiesterase 1; acid lysosomal (acid	
M81780	Homo sapiens acid sphingomyelinase (SMPD1) gene; complete cds; ORF's 1-3; complete cds's	
M81780	Homo sapiens acid sphingomyelinase (SMPD1) gene; complete cds; ORF's 1-3; complete cds's	
M83822	cell division cycle 4-like	
M86934	DNA segment; numerous copies; expressed probes (GS1 gene)	
M87338	replication factor C (activator 1) 2 (40kD)	
M96326	azurocidin 1 (cationic antimicrobial protein 37)	
M96954	TIA1 cytotoxic granule-associated RNA-binding protein-like 1	
M98833	Friend leukemia virus integration 1	
S66793	arrestin 3; retinal (X-arrestin)	
S72370	pyruvate carboxylase	
S78569	laminin; alpha 4	
S79873	lysosomal-associated membrane protein 2	
S83325	aspartate beta-hydroxylase	
S83364		
S83365		
U01212	olfactory marker protein (symbol provisional)	
U01922	translocase of inner mitochondrial membrane 8 (yeast) homolog A	
U02556	t-complex-associated-testis-expressed 1-like	
U02680	protein tyrosine kinase 9	
U03272	fibrillin 2(congenital contractural arachnodactyly)	
U04209	microfibrillar-associated protein 1	
U05237	fetal Alzheimer antigen	
U07225	purinergic receptor P2Y; G-protein coupled; 2	
U07620	mitogen-activated protein kinase 10	
U09759	mitogen-activated protein kinase 9	
U09820	alpha thalassemia/mental retardation syndrome X-linked	
U11313	sterol carrier protein 2	
U14518	centromere protein A (17kD)	
U14575	protein phosphatase 1; regulatory (inhibitor) subunit 8	
U15173	BCL2/adenovirus E1B 19kD-interacting protein 2	
U15932	dual specificity phosphatase 5	
U18291	CDC16 (cell division cycle 16; S. cerevisiae; homolog)	
U18300	damage-specific DNA binding protein 2 (48kD)	
U18383	nuclear respiratory factor 1	
U20536	caspase 6; apoptosis-related cysteine protease	
U21551	branched chain aminotransferase 1; cytosolic	
U23028	eukaryotic translation initiation factor 2B; subunit 5 (epsilon;	
U23752	SRY (sex-determining region Y)-box 11	
U25435	transcriptional repressor	
U25997	stanniocalcin	

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
U28251	zinc finger protein 169	
U28831		
U30245		
U32315	syntaxin 3A	
U32439	regulator of G-protein signalling 7	
U32849	N-myc (and STAT) interactor	
U35139	necdin (mouse) homolog	
U36764	eukaryotic translation initiation factor 3; subunit 2 (beta; 36kD)	
U39400	chromosome 11 open reading frame 4	
U39657	mitogen-activated protein kinase kinase 6	
U41344	proline arginine-rich end leucine-rich repeat protein	
U41766	a disintegrin and metalloproteinase domain 9 (meltrin gamma)	
U41813	homeo box A9	
U41815	nucleoporin 98kD	
U43286	selenophosphate synthetase 2	
U44378	MAD (mothers against decapentaplegic; Drosophila) homolog 4	
U44754	small nuclear RNA activating complex; polypeptide 1; 43kD	
U47011	fibroblast growth factor 8 (androgen-induced)	
U47011	fibroblast growth factor 8 (androgen-induced)	
U47011	fibroblast growth factor 8 (androgen-induced)	
U47011	fibroblast growth factor 8 (androgen-induced)	
U47077	protein kinase; DNA-activated; catalytic polypeptide	
U48251	protein kinase C binding protein 1	
U50535	Human BRCA2 region; mRNA sequence CG006	
U56833	von Hippel-Lindau binding protein 1	
U58091	cullin 4B	
U58837	cyclic nucleotide gated channel beta 1	
U59289	cadherin 13; H-cadherin (heart)	
U59863	TRAF family member-associated NFKB activator	
U67122	ubiquitin-like 1 (sentrin)	
U67319	caspase 7; apoptosis-related cysteine protease	
U68019	MAD (mothers against decapentaplegic; Drosophila) homolog 3	
U69611	a disintegrin and metalloproteinase domain 17 (tumor necrosis factor; alpha; converting enzyme)	
U70322	karyopherin (importin) beta 2	
U73524	ATP/GTP-binding protein	
U79267	protein phosphatase 4; regulatory subunit 1	
U79291	Human clone 23721 mRNA sequence	
U82671	Homo sapiens clone LM1955 H105e3 gene; partial cds	
U82671	zinc finger protein 185 (LIM domain)	
U84573	procollagen-lysine; 2-oxoglutarate 5-dioxygenase (lysine	
U90914	carboxypeptidase D	
U91316	cytosolic acyl coenzyme A thioester hydrolase	
U91932	adaptor-related protein complex 3; sigma 1 subunit	

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
U96131	Homo sapiens HPV16 E1 protein binding protein mRNA;	
U97018	echinoderm microtubule-associated protein-like	
U97188	IGF-II mRNA-binding protein 3	
V00503	collagen; type I; alpha 2	
X04327	2;3-bisphosphoglycerate mutase	
X06389	synaptophysin	
X07496	apolipoprotein A-I	
X07820	matrix metalloproteinase 10 (stromelysin 2)	
X14787	thrombospondin 1	
X15525	acid phosphatase 2; lysosomal	
X16396	methylene tetrahydrofolate dehydrogenase (NAD+ dependent); methenyltetrahydrofolate cyclohydrolase	
X16609	ankyrin 1; erythrocytic	
X53586	integrin; alpha 6	
X53586	integrin; alpha 6	
X53793	multifunctional polypeptide similar to SAICAR synthetase and AIR	
X54936	placental growth factor; vascular endothelial growth factor-related	
X55740	5' nucleotidase (CD73)	
X57025	insulin-like growth factor 1 (somatomedin C)	
X60673	adenylate kinase 3	
X60673	adenylate kinase 3	
X60708	dipeptidylpeptidase IV (CD26; adenosine deaminase complexing	
X62048	wee1+ (S. pombe) homolog	
X63097	Rhesus blood group; D antigen	
X63563	polymerase (RNA) II (DNA directed) polypeptide B (140kD)	
X64037	general transcription factor IIF; polypeptide 1 (74kD subunit)	
X69636	hect domain and RLD 2	
X69878	fms-related tyrosine kinase 4	
X70649	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1	
X72841	retinoblastoma-binding protein 7	
X74987	ATP-binding cassette; sub-family E (OABP); member 1	
X83107	BMX non-receptor tyrosine kinase	
X84194	acylphosphatase 1; erythrocyte (common) type	
X85753	cyclin-dependent kinase 8	
X87870	hepatocyte nuclear factor 4; alpha	
X89066	transient receptor potential channel 1	
X89398	uracil-DNA glycosylase	
X89398	uracil-DNA glycosylase	
X89399	RAS p21 protein activator (GTPase activating protein) 3	
X89426	endothelial cell-specific molecule 1	
X91247	thioredoxin reductase 1	
X91648	H.sapiens mRNA for pur alpha extended 3'untranslated region	

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
X92098	coated vesicle membrane protein	
X92110	H.sapiens mRNA for hcgVIII protein	
X94703	RAB28; member RAS oncogene family	
X96506	DR1-associated protein 1 (negative cofactor 2 alpha)	
X97230	killer cell immunoglobulin-like receptor; three domains; long	
X98263	M-phase phosphoprotein 6	
X98296	ubiquitin specific protease 9; X chromosome (Drosophila fat	
X99584	SMT3 (suppressor of mif two 3; yeast) homolog 1	
Y00264	amyloid beta (A4) precursor protein (protease nexin-II; Alzheimer	
Y07566	Ric (Drosophila)-like; expressed in many tissues	
Y07759	myosin VA (heavy polypeptide 12; myoxin)	
Y07827	butyrophilin; subfamily 3; member A1	
Y07867	Pirin	
Y09443	alkylglycerone phosphate synthase	
Y09858	H.sapiens mRNA for unknown protein	
Y12394	karyopherin alpha 3 (importin alpha 4)	
Z11559	iron-responsive element binding protein 1	
Z11695	mitogen-activated protein kinase 1	
Z15005	centromere protein E (312kD)	
Z46261	H3 histone family; member A	
AA011243	poly(rC)-binding protein 2	
AA018418	ESTs; Weakly similar to type-1 protein phosphatase skeletal muscle glycogen targeting subunit [H.sapiens]	
AA018758	ESTs	
AA018804	Homo sapiens clone 23675 mRNA sequence	
AA031993	SUMO-1 activating enzyme subunit 2	
AA044217	ESTs; Weakly similar to collagen alpha 2(I) chain [R.norvegicus]	
AA046548	SWI/SNF related; matrix associated; actin dependent regulator of chromatin; subfamily e; member 1	
AA057447	ESTs; Moderately similar to alternatively spliced product using	
AA058376	Sjogren syndrome antigen A2 (60kD; ribonucleoprotein	
AA083572	v-ral simian leukemia viral oncogene homolog A (ras related)	
AA085696		
AA088744	ESTs	
AA089688	EST	
AA091284	ESTs; Highly similar to HSPC030 [H.sapiens]	
AA092700	ESTs	
AA092968	ESTs	
AA094800	eukaryotic translation initiation factor 3; subunit 7 (zeta; 66/67kD)	
AA100219	ESTs	
AA114885	ESTs	

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
AA129547	met proto-oncogene (hepatocyte growth factor receptor)	
AA133016	ESTs	
AA149507	homolog of mouse quaking QKI (KH domain RNA binding protein)	
AA151005	sperm surface protein	
AA187101		
AA195179	eukaryotic translation initiation factor 4A; isoform 2	
AA203138	low density lipoprotein receptor (familial hypercholesterolemia)	
AA203645	Arg/Abl-interacting protein ArgBP2	
AA206236		
AA227621	ESTs; Weakly similar to weak similarity to collagens [C.elegans]	
AA248283	ESTs; Weakly similar to prostate-specific transglutaminase	
AA249611	SH3-binding domain glutamic acid-rich protein	
AA282640	ubiquitination factor E4B (homologous to yeast UFD2)	
AA287199	KIAA0081 protein	
AA313990	DKFZP564M112 protein	
AA314256	ESTs; Highly similar to CGI-94 protein [H.sapiens]	
AA314389	ADP-ribosylation factor-like 5	
AA324364	ESTs	
AA329211	NS1-associated protein 1	
AA399187	DKFZP434A043 protein	
AA421079	ESTs; Weakly similar to Sox-like transcriptional factor [H.sapiens]	
AA422029	ESTs	
AA425230	Ras-GTPase-activating protein SH3-domain-binding protein	
AA447052	KIAA0251 protein	
AA452000	Homo sapiens mRNA; cDNA DKFZp586E1624 (from clone	
AA456687	ESTs	
AA487015	Homo sapiens mRNA; cDNA DKFZp586L0120 (from clone	
AB002326	Human mRNA for KIAA0328 gene; partial cds	
-BioB-3		
C01527	ESTs	
C01714	serum-inducible kinase	
C01811	Homo sapiens clone 24921 mRNA sequence	
C02352	ESTs; Highly similar to CGI-121 protein [H.sapiens]	
C02375	ESTs	
C14448	EST	
D16611	coproporphyrinogen oxidase (coproporphyria; harderoporphyria)	
D25216	KIAA0014 gene product	
D31352	ESTs	
D58024	ESTs; Weakly similar to KIAA0768 protein [H.sapiens]	
D80897	KIAA1036 protein	
D82614	ESTs	

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
D87845	platelet-activating factor acetylhydrolase 2 (40kD)	
D89377	msh (Drosophila) homeo box homolog 2	
H06583	cAMP responsive element binding protein-like 2	
H40732	ESTs	
H46617	ESTs	
H56731	ESTs	
H75570	ESTs	
H78886	ESTs	
H81241	Kruppel-like factor 8	
L36531	integrin; alpha 8	
M63154	gastric intrinsic factor (vitamin B synthesis)	
M63180	threonyl-tRNA synthetase	
M91504	ESTs	
N56191	protocadherin 68	
N78483	ESTs; Weakly similar to F20D12.3 gene product [C.elegans]	
N79268	zinc finger protein 198	
R14652	Homo sapiens PAC clone DJ0872F07 from 7q31	
R20459	ESTs	
R22303	ESTs; Weakly similar to putative p150 [H.sapiens]	
R33779	ESTs; Weakly similar to p40 [H.sapiens]	
R36553	ESTs; Weakly similar to KIAA0681 protein [H.sapiens]	
R64534	ESTs	
R66475	ESTs	
R70621	KIAA0896 protein	
R79356	KIAA0544 protein	
R84933	ESTs	
AA007160	Homo sapiens mRNA; cDNA DKFZp564D016 (from clone	
AA007234	ESTs	
AA018409	ESTs	
AA025351	ESTs	
AA027168	KIAA0955 protein	
AA027317	ESTs	
AA029423	ESTs; Weakly similar to PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE [H.sapiens]	
AA031357	ESTs; Weakly similar to N-WASP [H.sapiens]	
AA045136	ESTs	
AA053400	ESTs	
AA055829	ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING	
AA065217	ESTs	
AA116054	ESTs; Weakly similar to KIAA0638 protein [H.sapiens]	
AA126311	ESTs	
AA129390	ESTs	
AA130273	ESTs; Weakly similar to hypothetical protein; similar to	

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
AA142919	ESTs	
AA150205	Kruppel-like factor 7 (ubiquitous)	
AA176867	ESTs	
AA180321	Homo sapiens (clone S164) mRNA; 3' end of cds	
AA180487	transforming; acidic coiled-coil containing protein 1	
AA187634	eukaryotic translation initiation factor 3; subunit 1 (alpha; 35kD)	
AA195399	ESTs	
AA234717	ESTs	
AA234743	ESTs	
AA234957	myotubularin related protein 1	
AA235604	Homo sapiens clone 25007 mRNA sequence	
AA236559	ESTs; Weakly similar to !!!! ALU SUBFAMILY SQ WARNING	
AA242868	ESTs; Weakly similar to house-keeping protein [M.musculus]	
AA251776	jun D proto-oncogene	
AA251909	budding uninhibited by benzimidazoles 1 (yeast homolog); beta	
AA252672	diptheria toxin resistance protein required for diphthamide biosynthesis (Saccharomyces)-like 2	
AA256157	ESTs	
AA256680	Homo sapiens mRNA; cDNA DKFZp564H1916 (from clone	
AA258873	ESTs	
AA262727	KIAA1033 protein	
AA281451	DKFZP564A043 protein	
AA281545	nuclear receptor co-repressor 1	
AA282069	KIAA0603 gene product	
AA283044	ESTs	
AA283930	ESTs	
AA284755	CDW52 antigen (CAMPATH-1 antigen)	
AA291268	DKFZP586L0724 protein	
AA291927	ESTs	
AA343514	ESTs	
AA398109	ESTs	
AA405737	ESTs	
AA406610	ESTs	
AA411465	ESTs; Moderately similar to HMG-box transcription factor	
AA416886	Homo sapiens mRNA; cDNA DKFZp564C1563 (from clone	
AA424013	Homo sapiens clone 23767 and 23782 mRNA sequences	
AA424148	DKFZP434I116 protein	
AA424558	phosducin-like	
AA424961	similar to S. cerevisiae SSM4	
AA425367	ESTs	
AA425921	ESTs	
AA426220	KIAA0523 protein	

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
AA427735	ESTs	
AA430673	ESTs	
AA432248	ESTs	
AA435896	ESTs	
AA436705	KIAA0766 gene product	
AA446561	KIAA0470 gene product	
AA448238	KIAA0915 protein	
AA448688	ESTs; Weakly similar to KIAA0638 protein [H.sapiens]	
AA449756	ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING	
AA450303	ESTs	
AA452411	ESTs; Highly similar to mediator [H.sapiens]	
AA454566	hemoglobin; gamma G	
AA454667	ESTs	
AA456437	ESTs	
AA456646	ESTs	
AA456826	ESTs	
AA456981	ESTs	
AA458959	ESTs	
AA459950	ESTs	
AA460449	ESTs; Highly similar to phosphoserine aminotransferase	
AA463910	ESTs	
AA464603	ESTs	
AA464606	MRS1 protein	
AA465093	TIA1 cytotoxic granule-associated RNA-binding protein	
AA465692	KIAA0648 protein	
AA476473	triple functional domain (PTPRF interacting)	
AA478109	ESTs	
AA478474	ESTs	
AA480889	ESTs	
AA485223	ESTs	
AA485254	ESTs	
AA486183	ESTs; Weakly similar to similar to oxysterol-binding proteins	
AA496936	ESTs	
AA598589	ESTs	
AA598831	ESTs	
AA600150	ESTs	
AA608545	RAD51 (S. cerevisiae) homolog (E coli RecA homolog)	
AA609210	ESTs	
AA610108	ESTs; Highly similar to CGI-124 protein [H.sapiens]	
AA620582	ESTs; Weakly similar to KIAA0869 protein [H.sapiens]	
AA621239	ESTs; Highly similar to ALG-2 interacting protein AIP1	
AA621714	ESTs	

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
AA621718	ESTs; Moderately similar to CGI-74 protein [H.sapiens]	
D19673	ESTs	
D25755	ESTs	
D51095	DKFZP586E1621 protein	
D60272	ESTs; Weakly similar to macrophage lectin 2 [H.sapiens]	
T08879	cathepsin F	
T34527	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1)	
T40327	lung resistance-related protein	
T62771	nucleophosmin/nucleoplasmin; 3	
T63174	Homo sapiens mRNA; cDNA DKFZp586I0324 (from clone	
T83444	KIAA0887 protein	
T93641	ESTs	
U48263	prepronociceptin	
U49065	interleukin 1 receptor-like 2	
U79300	Human clone 23629 mRNA sequence	
U88573	NBR2	
U93867	polymerase (RNA) III (DNA directed) (62kD)	
W01094	ESTs	
W01568	ESTs	
W26853	cartilage oligomeric matrix protein (pseudoachondroplasia; epiphyseal dysplasia 1; multiple)	
W27179	BCL2/adenovirus E1B 19kD-interacting protein 3-like	
W27965	EST	
W36280	NS1-associated protein 1	
W47063	ESTs	
W79060	isocitrate dehydrogenase 2 (NADP+); mitochondrial	
W88550	KIAA1058 protein	
X60486	H4 histone family; member G	
X78931	zinc finger protein 272	
Z14077	YY1 transcription factor	
AA002147	EST	
AA004711	ESTs	
AA010383	EST	
AA015761	ESTs	
AA018772	ESTs	
AA021473	EST	
AA024835	potassium voltage-gated channel; delayed-rectifier; subfamily S;	
AA025858	Homo sapiens mRNA; cDNA DKFZp586B1024 (from clone	
AA027229	ESTs; Weakly similar to F45E12.5 [C.elegans]	
AA029428	ESTs	
AA035143	ESTs	
AA035237	butyrate response factor 2 (EGF-response factor 2)	

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
AA039347	EST	
AA040740	ESTs	
AA041551	ESTs	
AA045513	ESTs	
AA045745	ESTs	
AA055348	ESTs	
AA056582	KIAA0372 gene product	
AA056697	ESTs	
AA056746	EST	
AA057678	ESTs	
AA058681	ESTs	
AA058686	ESTs	
AA062840		
AA064859		
AA065069		
AA069923		
AA070799	zinc finger protein 6 (CMPX1)	
AA070815		
AA075374		
AA076382		
AA078787	ESTs	
AA078986		
AA079393		
AA079487		
AA083207	EST	
AA083256		
AA084415		
AA085274		
AA088678	ESTs	
AA100925	stress-associated endoplasmic reticulum protein 1; ribosome associated membrane protein 4	
AA101255	Homo sapiens mRNA for H-2K binding factor-2; complete cds	
AA126474	stanniocalcin 2	
AA127017	ESTs	
AA129968	ESTs; Weakly similar to PROTEIN PHOSPHATASE PP2A; 130 KD REGULATORY SUBUNIT [H.sapiens]	
AA130240	ESTs	
AA131866	ESTs; Weakly similar to DY3.6 [C.elegans]	
AA132039	ESTs	
AA132983	DKFZP586G1517 protein	
AA133250	ESTs	
AA133583	high-mobility group (nonhistone chromosomal) protein isoform I-C	
AA135941	ESTs	
AA148650		

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
AA151110	ESTs	
AA155754	EST	
AA156125	ESTs; Moderately similar to hedgehog-interacting protein [M.musculus]	
AA156289	ESTs	
AA156997	ESTs	
AA157291	EST	
AA157293	ESTs	
AA164293	ESTs	
AA164676	ESTs; Weakly similar to weak similarity to S. cerevisiae intracellular protein transport protein US)1 [C.elegans]	
AA167375	KIAA0530 protein	
AA167550	Homo sapiens mRNA; cDNA DKFZp564M113 (from clone	
AA176589	EST	
AA180448	EST	
AA187144	endothelin 1	
AA189170	ESTs	
AA192757	ESTs	
AA205650	ESTs	
AA233342	ESTs; Weakly similar to WD40 protein Ciao 1 [H.sapiens]	
AA233472	ESTs	
AA234110	ESTs	
D80981	ESTs	
F01660	ESTs	
F02206	EST; Highly similar to ether-a-go-go-related protein [H.sapiens]	
F02208	ESTs	
F02544	ESTs	
F03918	ESTs	
F04258	pyrophosphatase (inorganic)	
F04600	ESTs	
F08998	ESTs	
F09605	ESTs	
F11115	ESTs	
H06371	Homo sapiens clone 24993 mRNA sequence	
H10995	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE	
H11938	ESTs; Highly similar to histone acetyltransferase [H.sapiens]	
H16568	ESTs	
H16772	ESTs	
H18951	ESTs; Moderately similar to dJ1163J1.1 [H.sapiens]	
H20859	ESTs	
H23747	ESTs	
H38087	ESTs; Weakly similar to NG22 [H.sapiens]	
H40331	ESTs	
H40567	ESTs	

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
H46966	ESTs	
H56640	ESTs	
H57154	ESTs; Weakly similar to organic anion transporter 1 [H.sapiens]	
H96712	ESTs	
N20814	ESTs	
N25249	synaptosomal-associated protein; 23kD	
N27100	keratin 5 (epidermolysis bullosa simplex;	
N39616	RNA (guanine-7-) methyltransferase	
N48982	ESTs	
N51957	ESTs	
N52271	LIM protein (similar to rat protein kinase C-binding enigma)	
N59435	ESTs; Highly similar to CGI-112 protein [H.sapiens]	
N64139	ESTs; Weakly similar to large tumor suppressor 1 [H.sapiens]	
N66981	ESTs	
N68640	ESTs	
N69352	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 15	
N95226	KIAA0758 protein	
R00138	ESTs	
R07998	ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING	
R08929	ubiquitin-conjugating enzyme E2G 2 (homologous to yeast UBC7)	
R10307	ESTs	
R33354	ESTs	
R36083	ESTs	
R37938	KIAA0440 protein	
R39330		
R40816	cullin 4A	
R43162	ESTs	
R45698	ESTs; Weakly similar to cAMP inducible 2 protein [M.musculus]	
R54554	ESTs	
R68425	ESTs	
R68568	ATX1 (antioxidant protein 1; yeast) homolog 1	
R68763	ESTs	
R70467	ESTs	
R73565	Homo sapiens mRNA; cDNA DKFZp564M113 (from clone	
R73640	ESTs	
R78376	EST	
R92453	EST	
T03865	ESTs	
T03872	ESTs	
T10072	ESTs	
T10080	ESTs	
T10132	KIAA0478 gene product	

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
T15343	ESTs	
T23457	ESTs	
T23555	ESTs	
T23670	ESTs	
T23948	ESTs	
T33464	ESTs	
T34413	ESTs	
T34611	ESTs	
T40920	ESTs	
T55182	ESTs; Highly similar to IGF-II mRNA-binding protein 2 [H.sapiens]	
T77453	ESTs	
T84039	ESTs	
T86458	ESTs	
T87693	EST	
T89350	ESTs	
T90945	ESTs	
T90987	ESTs	
T91863	ESTs	
T91881	KIAA0563 gene product	
T93783	ESTs	
T96687	ESTs	
T96944	Homo sapiens mRNA; cDNA DKFZp434H132 (from clone	
T97307	ESTs; Moderately similar to !!!! ALU SUBFAMILY J WARNING	
T97764	ESTs	
W48817	ESTs	
W58343	DKFZP586B2420 protein	
W59949	ESTs; Moderately similar to GTP-BINDING PROTEIN TC10	
W74644	ESTs	
W74761	ESTs; Highly similar to ubiquitin-conjugating enzyme HBUCE1	
W74802	ESTs	
W81205	ESTs	
W81237	ESTs	
W90146	ESTs	
W92798	ESTs	
Z38412	EST	
Z38709	inositol 1;4;5-triphosphate receptor; type 2	
Z38904	ESTs; Weakly similar to KIAA0970 protein [H.sapiens]	
Z39103	core-binding factor; runt domain; alpha subunit 2; translocated to;	
Z39930	calreticulin	
Z39939	ESTs	
Z40012	NCK-associated protein 1	
Z40377	ESTs	

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
Z40820	ESTs	
Z41680	Homo sapiens mRNA; cDNA DKFZp566P013 (from clone	
-BioB-3		
AA005112	LIM domain only 7	
AA005432	DKFZP547E2110 protein	
AA010163	upstream regulatory element binding protein 1	
AA026356	ESTs	
AA026901	ESTs	
AA036867	ESTs; Weakly similar to coded for by C. elegans cDNA yk30b3.5	
AA044644	lymphocyte-specific protein 1	
AA046426	Cdc42 effector protein 3	
AA054515	ESTs; Weakly similar to prostate-specific transglutaminase	
AA084162		
AA085749	ATP binding protein associated with cell differentiation	
AA098874	DKFZP434I116 protein	
AA101056		
AA102746	ESTs	
AA114250	KIAA0512 gene product	
AA126561	stanniocalcin	
AA128980	ESTs	
AA129757	ESTs; Weakly similar to 60S RIBOSOMAL PROTEIN L22	
AA129921	S-adenosylhomocysteine hydrolase-like 1	
AA133331	KIAA0741 gene product	
AA135958	ESTs	
AA136524	eukaryotic translation elongation factor 1 alpha 1	
AA147044	ESTs; Weakly similar to !!!! ALU CLASS C WARNING ENTRY !!!!	
AA148885	minichromosome maintenance deficient (S. cerevisiae) 4	
AA150043	ESTs	
AA151621	ESTs	
AA155743	ferritin; light polypeptide	
AA156335	ESTs	
AA156336	nuclear receptor co-repressor 1	
AA159181	ESTs; Weakly similar to Lpa8p [S.cerevisiae]	
AA159825	ESTs; Weakly similar to ORF YNL227c [S.cerevisiae]	
AA234185	ESTs	
AA234929	ESTs	
AA234935	ESTs	
AA236359	ESTs	
AA236466	ESTs	
AA236535	Human clone 23654 mRNA sequence	
AA236935	Human normal keratinocyte mRNA	
AA236942	ESTs	

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
AA237018	ESTs	
AA237025	ESTs	
AA242751	KIAA0903 protein	
AA242760		
AA242763	CDC14 (cell division cycle 14; S. cerevisiae) homolog B	
AA242809	ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING	
AA243133	serine/threonine kinase 15	
AA243495	lectin; mannose-binding; 1	
AA243706	ESTs	
AA250848	ESTs	
AA250868	ESTs	
AA251152	ESTs	
AA251544	ESTs	
AA251792	fatty-acid-Coenzyme A ligase; long-chain 4	
AA252063	BH-protocadherin (brain-heart)	
AA252144	ESTs	
AA252524		
AA253461	ESTs	
AA255522	ESTs; Weakly similar to INHIBITOR OF APOPTOSIS PROTEIN 1	
AA256468	ESTs	
AA256528	ESTs	
AA257976	ESTs	
AA258296	KIAA0579 protein	
AA258409	myelin protein zero-like 1	
AA258421	hypothetical protein	
AA262077	aldehyde dehydrogenase 5 family; member A1	
AA278650	ESTs; Weakly similar to similar to the beta transducin family	
AA278766	ESTs	
AA279667	natural killer-tumor recognition sequence	
AA280791	eukaryotic translation initiation factor 5	
AA280819	MADS box transcription enhancer factor 2; polypeptide C	
AA280828	Homo sapiens mRNA; cDNA DKFZp586M141 (from clone	
AA282195	ESTs; Weakly similar to Unknown [H.sapiens]	
AA283127	Homo sapiens clone LM1955 H105e3 gene; partial cds	
AA284694	nucleoporin-like protein 1	
AA291137	ESTs	
AA291708	ESTs; Weakly similar to !!!! ALU SUBFAMILY SQ WARNING	
AA293495	chromosome 8 open reading frame 1	
AA347193	ESTs.	
AA398474	Homo sapiens mRNA; cDNA DKFZp586H051 (from clone	
AA398512	ESTs	

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
AA400277	ESTs	
AA400896	ESTs	
AA404494	CTP synthase	
AA410345	ESTs; Weakly similar to junctional adhesion molecule [H.sapiens]	
AA416733	ESTs; Weakly similar to !!!! ALU SUBFAMILY SC WARNING	
AA425154	ESTs	
AA426573	ESTs; Moderately similar to endomucin [M.musculus]	
AA431418	N-acetylglucosaminidase; alpha- (Sanfilippo disease IIIB)	
AA436182	Human DNA sequence from clone 44A20 on chromosome 6q23.1-24.3. Contains a gene for a novel protein similar to MTHFD1 (methylenetetrahydrofolate dehydrogenase (NADP+ dependent); methenyltetrahydrofolate cyclohydrolase;	
AA437099	ESTs	
AA446585	ESTs	
AA446887	ESTs	
AA447224	ESTs; Weakly similar to cDNA EST CEESW54F comes from this	
AA447709	ESTs; Moderately similar to putative transcription factor CA150	
AA453624	deoxynucleotidyltransferase; terminal	
AA455044	ESTs	
AA456045	ESTs	
AA460454	ESTs; Weakly similar to KIAA0512 protein [H.sapiens]	
AA476494	ESTs; Weakly similar to KIAA0512 protein [H.sapiens]	
AA476738	leucine rich repeat (in FLII) interacting protein 1	
AA481422	Homo sapiens mRNA for H-2K binding factor-2; complete cds	
AA482269	integral membrane protein 1	
AA482595	ESTs; Weakly similar to F25B5.3 [C.elegans]	
AA485084	ESTs	
AA485431	ESTs	
AA489057	stromal antigen 2	
AA489638	DKFZP564M2423 protein	
AA491000	Homo sapiens mRNA; cDNA DKFZp586N1720 (from clone	
AA491250	ESTs	
AA505133	solute carrier family 2 (facilitated glucose transporter); member 3	
AA598447	exportin; tRNA (nuclear export receptor for tRNAs)	
AA599243	general transcription factor IIIA	
AA599574	lipase; endothelial	
AA600153	DEK oncogene (DNA binding)	
AA609309	ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING	
AA609710	Human chromosome 3p21.1 gene sequence	
AA610068	PIBF1 gene product	
AA621399	ESTs	
AA621752	26S proteasome-associated pad1 homolog	

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
C21523	ESTs	
D12160	ESTs; Moderately similar to !!!! ALU SUBFAMILY J WARNING	
D19708	ESTs	
D25801	ESTs; Highly similar to KIAA0445 protein [H.sapiens]	
D45652	a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif; 4; aggrecan 1	
D60208	ESTs	
D80504	zinc finger protein 198	
F03010	myeloid/lymphoid or mixed-lineage leukemia 2	
F04247	ESTs	
F10966	Homo sapiens mRNA; cDNA DKFZp434M196 (from clone	
F13700	ribonuclease P; 40kD subunit	
H05063	ESTs; Weakly similar to /prediction	
H16758	erythropoietin receptor	
H17315	EST	
H22556	putative translation initiation factor	
H22566	ESTs	
H48459	KIAA0186 gene product	
H53073		
H56559	KIAA0601 protein	
H57957	EST	
H64938	ESTs	
H64973	ESTs	
H69535	ESTs	
H73110	ESTs	
H81783	ESTs	
H86259	Homo sapiens chromosome 19; cosmid R32611	
H88353	ESTs; Weakly similar to line-1 protein ORF2 [H.sapiens]	
H88639	YY1-associated factor 2	
H88675	nuclear receptor co-repressor 1	
H93708	sperm specific antigen 2	
N22107	ESTs	
N24046	ESTs	
N27028	ESTs	
N30205	ESTs	
N30621	ESTs	
N33258	nuclear receptor co-repressor 1	
N33390	EST	
N40180	EST	
N45198	EST; Highly similar to similar to Cdc14B1 phosphatase [H.sapiens]	
N45979	SH3 domain protein 1B	
N48325	EST	

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
N48913	ESTs	
N49394	KIAA0716 gene product	
N50656	ESTs; Highly similar to mosaic protein LR11 [H.sapiens]	
N50721	signal sequence receptor; gamma (translocon-associated protein	
N53143	Homo sapiens clone 25218 mRNA sequence	
N53359	ESTs; Weakly similar to beta-TrCP protein E3RS-IkappaB	
N55326	ESTs	
N55493		
N57493	EST	
N62955	ESTs; Weakly similar to KIAA0396 [H.sapiens]	
N63520	EST	
N63604	ESTs	
N64166	frizzled (Drosophila) homolog 7	
N64168	ESTs	
N64191	ESTs	
N66845	ESTs; Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!!	
N67135	ESTs	
N67295	ESTs	
N68399	H2B histone family; member N	
N68963	ESTs	
N69331	peptidylprolyl isomerase C (cyclophilin C)	
N70777	ESTs	
N71364	ESTs	
N71545	ESTs	
N71571	ESTs	
N74456	EST	
N75594	ESTs	
N79035	ESTs	
N80279	hypothetical protein	
N91797	ESTs	
N92454	karyopherin (importin) beta 1	
N94581	actin; beta	
N94746	ESTs	
N98238	ESTs	
R02384	ESTs	
R16833	ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]	
R41828	myosin VA (heavy polypeptide 12; myoxin)	
R43203	EST	
R46395	DKFZP566A0946 protein	
R58863	ESTs	
R78248	ESTs; Weakly similar to KIAA0970 protein [H.sapiens]	
T11483	ESTs	

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
T16896	ESTs	
T23820	cyclin T2	
T30222	ESTs; Moderately similar to tetracycline transporter-like protein	
W15275	Homo sapiens mRNA; cDNA DKFZp586E1624 (from clone	
W38194		
W42414	MAD (mothers against decapentaplegic; Drosophila) homolog 3	
W46577	endothelial cell-specific molecule 1	
W49632	Human clone 23908 mRNA sequence	
W57613	ESTs	
W57759	EST	
W61118	ESTs	
W65344	ESTs; Moderately similar to hypothetical protein [H.sapiens]	
W69216	ESTs	
W69379	Homo sapiens mRNA; cDNA DKFZp586D0923 (from clone	
W86728	ESTs	
Z38499	MKP-1 like protein tyrosine phosphatase	
Z38630	bladder cancer related protein (10kD)	
Z39494	ESTs	
Z39623	ESTs	
Z40071	BMX non-receptor tyrosine kinase	
Z40174	ESTs	
Z40182	EST	
Z40904	EST	
AA166965	ESTs	
AA167500	EST	
AA169599	ESTs	
AA171724	ESTs; Weakly similar to ORF YNL059c [S.cerevisiae]	
AA171739	ESTs	
AA177105	ESTs; Weakly similar to MITOCHONDRIAL CARNITINE/ACYLCARNITINE CARRIER PROTEIN [H.sapiens]	
AA182626	ESTs	
AA186324	cell cycle progression 8 protein	
AA192099	zinc finger protein 148 (pHZ-52)	
AA192173	ESTs	
AA192415	ESTs	
AA192553	ESTs; Highly similar to RGC-32 [R.norvegicus]	
AA194851	ESTs	
AA195520	ESTs	
AA196300	ESTs; Weakly similar to alternatively spliced product using exon	
AA196517	protease; serine; 15	
AA196549	ESTs	
AA196721		

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
AA196729	ESTs	
AA196979	ESTs; Weakly similar to protease [H.sapiens]	
AA206828		
AA207123	immunoglobulin superfamily; member 3	
AA214539	TIA1 cytotoxic granule-associated RNA-binding protein	
AA226914	nuclear receptor subfamily 2; group C; member 1	
AA227260	Zic family member 3 (odd-paired Drosophila homolog; heterotaxy	
AA227469	EST	
AA233122	ESTs; Highly similar to multifunctional calcium/calmodulin-dependent protein kinase II delta2 isoform	
AA233334	Machado-Joseph disease (spinocerebellar ataxia 3; olivopontocerebellar ataxia 3; autosomal dominant; ataxin 3)	
AA233347	zinc finger protein 216	
AA233519	ESTs; Weakly similar to evectin-1 [R.norvegicus]	
AA233714	Apg12 (autophagy 12; S. cerevisiae)-like	
AA233796	eukaryotic translation initiation factor 4E	
AA235050	ESTs	
AA235704	ESTs; Weakly similar to Wiscott-Aldrich Syndrome protein	
AA236031	ESTs	
AA236352	ESTs	
AA236390	ESTs	
AA236453	ESTs	
AA243370	EST	
AA250947	ESTs	
AA251083	ESTs	
AA251113	ESTs	
AA251973	ESTs	
AA252023	ESTs; Weakly similar to HRIHFB2157 [H.sapiens]	
AA252414	ESTs	
AA252650	mitogen-activated protein kinase kinase 7	
AA255523	ESTs	
AA258128	ESTs	
AA262105	Homo sapiens mRNA; cDNA DKFZp564L1916 (from clone	
AA262107	ESTs	
AA262235	ESTs	
AA278298	M-phase phosphoprotein 1	
AA278529	serine/threonine kinase 18	
AA278721	ESTs	
AA280036	eukaryotic translation initiation factor 4A; isoform 2	
AA280648	ESTs; Weakly similar to rab-related GTP-binding protein	
AA280738	ESTs	
AA280794	ESTs	

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
AA280837	ESTs	
AA280886	ESTs	
AA280934	ESTs	
AA281535	KIAA0879 protein	
AA281797	general transcription factor IIH; polypeptide 2 (44kD subunit)	
AA282047	ESTs	
AA283002	zinc finger protein 187	
AA283709	calpain like protease	
AA283902	ESTs	
AA284108	Human DNA from chromosome 19-specific cosmid F25965;	
AA284109	Human DNA sequence from clone 71L16 on chromosome Xp11. Contains a probable Zinc Finger protein (pseudo)gene; an unknown putative gene; a pseudogene with high similarity to part	
AA284371	interleukin 13 receptor; alpha 1	
AA284744	ESTs; Highly similar to prefoldin subunit 2 [M.musculus]	
AA284784	mitochondrial ribosome recycling factor	
AA284840	ESTs	
AA286844	ESTs	
AA287032	ESTs	
AA287038	ESTs	
AA287546	ESTs	
AA287553	ESTs	
AA287556	ESTs; Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!!	
AA287564	IDN3 protein	
AA291015	CDC7 (cell division cycle 7; S. cerevisiae; homolog)-like 1	
AA291716	ESTs	
AA291749	estrogen receptor 1	
AA293656	ESTs	
AA302430	Human DNA sequence from clone 141H5 on chromosome Xq22.1-23. Contains parts of a novel Chordin LIKE protein with von Willebrand factor type C domains. Contains ESTs; STSs and	
AA302809	EST	
AA302820	purinergic receptor P2X; ligand-gated ion channel; 4	
AA310499	ESTs	
AA321890		
AA340589	EST	
AA340622	ESTs	
AA342457	ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WARNING	
AA342828	glycoprotein V (platelet)	
AA342864	ESTs	
AA342973	ESTs	
AA346495	ESTs	
AA347573	fibronectin leucine rich transmembrane protein 2	

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
AA347614	ESTs	
AA347717	ESTs	
AA348913	ESTs	
AA349647	EST	
AA349773	ESTs	
AA350541	ESTs	
AA357159	EST	
AA357172	ESTs	
AA369856	vacuolar protein sorting 41 (yeast homolog)	
AA370132	EST	
AA370472	ESTs	
AA370867	ESTs	
AA377296	ESTs	
AA383902	ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING	
AA385934	EST; Highly similar to predicted using Genefinder [C.elegans]	
AA386255	EST	
AA386260	EST	
AA386266	ESTs; Weakly similar to M6a [H.sapiens]	
AA398014	ESTs	
AA398222	ESTs	
AA398235	ESTs	
AA398348	ESTs	
AA398482	EST	
AA398504	ESTs	
AA398505	ESTs	
AA398507	nucleoporin 50kD	
AA398523	ESTs	
AA398625	ESTs	
AA398632	ESTs	
AA398633	ESTs	
AA398894	ESTs	
AA398895	EST	
AA398900	ESTs	
AA398904	EST	
AA399122	ESTs; Weakly similar to mitochondrial citrate transport protein	
AA399371	ESTs; Weakly similar to zinc finger protein SALL1 [H.sapiens]	
AA399373	ESTs; Highly similar to KIAA0568 protein [H.sapiens]	
AA399441	ESTs	
AA399636	ESTs	
AA399640	ESTs	
AA399680	ESTs	
AA400080	ESTs	
AA400262	ESTs	

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
AA400725	ESTs	
AA400748	Homo sapiens mRNA; cDNA DKFZp434D024 (from clone	
AA400780	ESTs	
AA401631	ESTs	
AA401688	ESTs	
AA401695	EST	
AA402227	ESTs; Weakly similar to TROPOMODULIN [H.sapiens]	
AA402329	phosphodiesterase 4A; cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E2)	
AA402398	ESTs	
AA402449	EST	
AA402468	ESTs	
AA403268	ESTs	
AA403314	ESTs	
AA404229	EST	
AA404260	ESTs	
AA404271	glutamate receptor; ionotropic; kainate 1	
AA405026	ESTs	
AA405182	ESTs	
AA405237		
AA406061	EST	
AA406063	ESTs	
AA406070	EST	
AA406137	EST	
AA406335	ESTs	
AA411801	KIAA0307 gene product	
AA411804	ESTs	
AA411833	ESTs; Highly similar to Trad [H.sapiens]	
AA412219	ESTs	
AA412259	ESTs	
AA412497	EST	
AA412498	ESTs	
AA416586	ESTs	
AA416867	EST	
AA416874	ESTs	
AA421133	ESTs	
AA421138	EST	
AA422079	ESTs; Weakly similar to RAR-RESPONSIVE PROTEIN TIG1	
AA423837	ESTs	
AA424328	ESTs	
AA424339	ESTs	
AA424469	ESTs	
AA424502	ESTs	

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
AA425004	ESTs	
AA425734	ESTs; Weakly similar to hypothetical protein [H.sapiens]	
AA425887	ESTs	
AA426456	ESTs	
AA427396	ESTs	
AA427555	KIAA0203 gene product	
AA428218	ESTs	
AA428242	transcription factor 9 (binds GC-rich sequences)	
AA428281	EST	
AA428865	EST	
AA428994	ESTs	
AA429666	ESTs	
AA430181	ESTs	
AA430184	ATP/GTP-binding protein	
AA431288	CD3D antigen; delta polypeptide (TiT3 complex)	
AA431293	ESTs	
AA431478	ESTs	
AA431492	EST	
AA431732	EST	
AA432278	ESTs	
AA434411	ESTs	
AA435512	ESTs	
AA435698	ESTs	
AA435711	KIAA0712 gene product	
AA435815	Clk-associating RS-cyclophilin	
AA435842	ESTs	
AA436475	ESTs	
AA436489	ESTs	
AA442060	ESTs	
AA442079	ESTs	
AA443151	ESTs; Weakly similar to weak similarity with quinone	
AA446133	ESTs	
AA447145	Homo sapiens KIAA0399 mRNA; partial cds	
AA447398	EST	
AA447643	ESTs	
AA447742	dynein; axonemal; heavy polypeptide 17-like	
AA448226		
AA448825	EST	
AA449444	ESTs	
AA450087	regulator of Gz-selective protein signaling	
AA450211	EST	
AA450244	ESTs	
AA452123	ESTs; Weakly similar to T-complex protein 10A [H.sapiens]	
AA452155	zinc finger protein 198	

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
AA452156	EST	
AA453036	ESTs; Weakly similar to similar to molybdoterin biosynthesis	
AA453526	ESTs	
AA454085	EST	
AA454103	ESTs	
AA454642	ESTs	
AA454935	nuclear respiratory factor 1	
AA456323	ESTs	
AA457395	ESTs	
AA458850		
AA459662	ESTs	
AA459668	3-hydroxyisobutyryl-Coenzyme A hydrolase	
AA459679	ESTs; Weakly similar to The KIAA0191 gene is expressed	
AA459702	ESTs	
AA460017	ESTs; Weakly similar to diaphanous-related formin [M.musculus]	
AA460324	ESTs	
AA461509	ESTs; Weakly similar to putative p150 [H.sapiens]	
AA464414	ESTs	
AA464428	ESTs	
AA470084	ESTs	
AA476606	ESTs	
AA478521	ESTs	
AA478523	ESTs; Moderately similar to !!!! ALU SUBFAMILY J WARNING	
AA479949	RAB2; member RAS oncogene family	
AA481252	oncogene TC21	
AA485351	KIAA1067 protein	
AA487264	ESTs	
AA489072	KIAA0870 protein	
AA489630	KIAA0665 gene product	
AA490225	ESTs	
AA490227	ESTs	
AA490255	ESTs	
AA490890	ESTs	
AA490916	ESTs	
AA490925	epilepsy; progressive myoclonic epilepsy; type 2 gene; Lafora	
AA490955	ESTs; Weakly similar to bullous pemphigoid antigen [M.musculus]	
AA495812	ESTs	
AA495824	ESTs	
AA496369	ESTs	
AA504125	ESTs	
AA521473	SEC10 (S. cerevisiae)-like 1	

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
AA598440	EST	
AA598899	Homo sapiens mRNA; cDNA DKFZp564D036 (from clone	
AA599244	KIAA0530 protein	
AA599694	KIAA0133 gene product	
AA600037	ESTs	
AA609135	ESTs	
AA609582	katanin p60 (ATPase-containing) subunit A 1	
AA609684	ESTs	
AA609839	4-nitrophenylphosphatase domain and non-neuronal SNAP25-like	
AA609862	RNA-binding protein gene with multiple splicing	
AA620423	EST	
AA620747	ESTs	
AA621364	ESTs	
C20653	ESTs	
D20085	ESTs; Weakly similar to KIAA0742 protein [H.sapiens]	
D20749	ESTs	
D51285	ESTs	
D59972	cullin 5	
F04112	ESTs	
F13604	ESTs	
H01662	ESTs	
H05135	ESTs	
H12245		
H22842	EST	
H30894	ESTs	
H43442	leucyl-tRNA synthetase; mitochondrial	
H45996	putative G protein-coupled receptor	
H69281	ESTs	
H69485	ESTs	
H69899	ESTs; Moderately similar to unknown [H.sapiens]	
H70627	ESTs; Weakly similar to !!!! ALU CLASS E WARNING ENTRY !!!!	
H73050	Rhesus blood group; D antigen	
H73260	ESTs	
H77531	HIR (histone cell cycle regulation defective; S. cerevisiae)	
H80552	EST	
H80737	lysyl oxidase	
H93412	ESTs; Weakly similar to ORF YGR101w [S.cerevisiae]	
H94892	v-ral simian leukemia viral oncogene homolog A (ras related)	
H95643	neurotrophic tyrosine kinase; receptor; type 1	
H96552	ESTs	
H97146	ESTs; Highly similar to G protein-coupled receptor kinase 6;	
H99131	ESTs	

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
H99462	ribosomal protein; mitochondrial; L12	
H99837	ESTs	
N22140	ESTs; Weakly similar to beta-tubulin [H.sapiens]	
N22197	Sec23-interacting protein p125	
N23756	solute carrier family 23 (nucleobase transporters); member 1	
N24134	eukaryotic translation initiation factor 1A; Y chromosome	
N24195	novel centrosomal protein RanBPM	
N26739	DKFZP564B147 protein	
N27098	EST	
N27637	ESTs	
N33090	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 19 (Dbp5; yeast;	
N35967	serine/threonine kinase 24 (Ste20; yeast homolog)	
N38959	chaperonin containing TCP1; subunit 2 (beta)	
N39069	ESTs	
N46441	ESTs	
N48270	ESTs	
N48365	ESTs	
N51316	ESTs	
N51499	A kinase (PRKA) anchor protein 2	
N53976	ESTs	
N54157	ESTs	
N54300	ESTs	
N54831	ESTs	
N59849	ESTs	
N62132	ESTs	
N62375	EST	
N63138	ESTs	
N63172	cell division cycle 42 (GTP-binding protein; 25kD)	
N63772	novel putative protein similar to YIL091C yeast hypothetical 84 kD protein from SGA1-KTR7	
N63787	sema domain; immunoglobulin domain (Ig); short basic domain;	
N68168		
N68201	ESTs	
N68300	ESTs	
N68321	EST	
N69575	EST	
N75007	ESTs; Moderately similar to KIAA1004 protein [H.sapiens]	
N75542	transcription factor 4	
N90066	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl	
N91246	ESTs	
N92751	ESTs; Weakly similar to MICROTUBULE-ASSOCIATED	
N93214	KIAA0318 protein	

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
N99148	ESTs; Weakly similar to ZINC FINGER PROTEIN 83 [H.sapiens]	
R07876	ESTs; Weakly similar to unknown [S.cerevisiae]	
R10865	alpha-fetoprotein	
R11056	ESTs	
R11488	ESTs	
R22947	ESTs	
R23930	ESTs; Highly similar to prediabetic NOD sera-reactive autoantigen	
R26589	ESTs	
R37588	RAB2; member RAS oncogene family-like	
R37613	Homo sapiens clone 25027 mRNA sequence	
R38398	Homo sapiens clone 23758 mRNA sequence	
R39179	ESTs	
R40923	ESTs	
R41179	Human mRNA for KIAA0328 gene; partial cds	
R41294	ESTs	
R42307	early development regulator 2 (homolog of polyhomeotic 2)	
R43189	ESTs	
R43306	ESTs	
R44357	ESTs; Weakly similar to cDNA EST EMBL:T01421 comes from	
R44519	EST; Moderately similar to Pro-Pol-dUTPase polyprotein	
R45088		
R47948	ESTs	
R51524	ESTs	
R54950	ESTs	
R55241	ESTs	
R59585	ESTs	
R60044	ESTs; Highly similar to BETA-CATENIN [H.sapiens]	
R60872	ESTs	
R66690	ESTs	
R67266	exostoses (multiple)-like 1	
R73588	ESTs	
R79403	ESTs	
R87647	ESTs	
R93622	eukaryotic translation initiation factor 2; subunit 2 (beta; 38kD)	
R99599	heterogeneous nuclear ribonucleoprotein U (scaffold attachment	
R99612	ESTs; Moderately similar to !!!! ALU SUBFAMILY J WARNING	
T02888		
T03170	EST	
T10465		
T15418	EST	
T15597	KIAA0661 gene product	
T15652	ESTs	

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
T16898	ash2 (absent; small; or homeotic; Drosophila; homolog)-like	
T26644	ESTs; Weakly similar to zinc finger protein [H.sapiens]	
T40841	ESTs	
T47566		
T50116		
T50145		
T58615	ESTs	
T59940	ESTs	
T63595	ESTs	
T64891		
T64924	ESTs	
T64933	ESTs; Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]	
T68875		
T69027	ESTs	
T69924		
T70353	ESTs	
T79780	ESTs; Weakly similar to CGI-69 protein [H.sapiens]	
T79951	ESTs	
T80174	ESTs; Moderately similar to similar to NEDD-4 [H.sapiens]	
T80622	ESTs; Weakly similar to envelope [H.sapiens]	
T85352	ESTs	
T85373	ESTs	
T86284	ESTs	
T89579	transcription factor Dp-1	
T90360	ESTs	
T94328	ESTs	
T95590		
T97257	ESTs	
T97599	ESTs	
T97620	ESTs	
T97775	EST	
T98152	fibrillin 2(congenital contractural arachnodactyly)	
W31479	ESTs	
W37999	ESTs	
W38240		
W40150	chondroitin sulfate proteoglycan 6 (bamacan)	
W45435	KIAA0784 protein	
W58202	ESTs	
W58344	ESTs	
W58650	ESTs	
W68736	Human DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3; EC 1.6.99.3; CI-MLRQ); Tubulin Beta and Proto-oncogene Tyrosine-protein Kinase FER (EC 2.7.1.112;	

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
W69106	chromobox homolog 3 (Drosophila HP1 gamma)	
W69111	ESTs	
W69385	nuclear mitotic apparatus protein 1	
W69399	H1 histone family; member 0	
W69459	sex comb on midleg (Drosophila)-like 1	
W72424	S100 calcium-binding protein A9 (calgranulin B)	
W72724	ESTs	
W72834	ESTs	
W73955	Homo sapiens chromosome 19; cosmid R26445	
W74701	ESTs	
W76540	DKFZP564G2022 protein	
W79397	ESTs	
W85888	ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WARNING	
W86038	ESTs	
W86881	ESTs	
W87804	ESTs	
W88942		
W90022	ESTs; Highly similar to LECT2 precursor [H.sapiens]	
W92272	chromodomain helicase DNA binding protein 3	
W92764	tumor necrosis factor; alpha-induced protein 6	
W93040	Homo sapiens paired mesoderm homeo box 1 (PMX1); mRNA	
W93092	neutral sphingomyelinase (N-SMase) activation associated factor	
W93227	EST	
W93523	ESTs	
W93659	ESTs	
W94003	ESTs	
W94401	ESTs	
W94688	perilipin	
W94787	destrin (actin depolymerizing factor)	
Z38294	ESTs	
Z38311	ESTs	
Z38465	ESTs	
Z38525	ESTs	
Z38538	ESTs	
Z38551	ESTs	
Z38783	Ca2+-dependent activator protein for secretion	
Z39113	ESTs	
Z39255	YDD19 protein	
Z39591	EST	
Z39783	ESTs; Weakly similar to K01H12.1 [C.elegans]	
Z39920	ESTs; Weakly similar to NADH-CYTOCHROME B5 REDUCTASE	
Z40166	ESTs	
Z40388	ESTs	

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
Z40646	ESTs	
Z41697	ESTs	
Z99349	ESTs	
Z99394	zinc finger protein 36 (KOX 18)	

TABLE 4

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
D86425	Homo sapiens mRNA for nidogen-2	Hs.82733
D86983	Human mRNA for KIAA0230 gene; partial cds	Hs.118893
HG1098-HT1098	Cystatin D	
HG1103-HT1103	Guanine Nucleotide-Binding Protein Ral, Ras-Oncogene Related	
HG3342-HT3519	Id1	
J03764	plasminogen activator inhibitor; type I	Hs.82085
L06797	chemokine (C-X-C motif); receptor 4 (fusin)	Hs.89414
L15388	Human G protein-coupled receptor kinase (GRK5) mRNA, complete cds	Hs.211569
L20971	phosphodiesterase 4B; cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E4)	Hs.188
L35545	endothelial cell protein C/activated protein C receptor	Hs.82353
L76380	calcitonin receptor-like	Hs.152175
M21305	Human alpha satellite and satellite 3 junction DNA sequence	Hs.247946
M24736	selectin E (endothelial adhesion molecule 1)	Hs.89546
M31166	pentaxin-related gene; rapidly induced by IL-1 beta	Hs.2050
M31551	plasminogen activator inhibitor; type II (arginine-serpin)	Hs.75716
M32334	intercellular adhesion molecule 2	Hs.83733
M61916	laminin; beta 1	Hs.82124
M68874	Human phosphatidylcholine 2-acylhydrolase (cPLA2) mRNA, complete cds	
M74719	transcription factor 4	Hs.75356
M92934	connective tissue growth factor	Hs.75511
M94856	fatty acid binding protein 5 (psoriasis-associated)	Hs.153179
U03057	singed (Drosophila)-like (sea urchin fascin homolog like)	Hs.118400
U03877	EGF-containing fibulin-like extracellular matrix protein 1	Hs.76224
U18300	damage-specific DNA binding protein 2 (48kD)	Hs.77602
U27109	Human prepromultimerin mRNA; complete cds	Hs.32934
U31384	guanine nucleotide binding protein 11	Hs.83381
U33053	protein kinase C-like 1	Hs.2499
U59423	MAD (mothers against decapentaplegic; Drosophila) homolog 1	Hs.79067
U70322	karyopherin (importin) beta 2	Hs.168075
U81607	kinase scaffold protein gravin	Hs.788
U83463	syndecan binding protein (syntenin)	Hs.8180
U89942	lysyl oxidase-like 2	Hs.83354
X04729	Human mRNA for plasminogen activator inhibitor type 1 N-terminus	
X06256	integrin; alpha 5 (fibronectin receptor; alpha polypeptide)	Hs.149609
X07820	matrix metalloproteinase 10 (stromelysin 2)	Hs.2258
X54925	matrix metalloproteinase 1 (interstitial collagenase)	Hs.83169
X54936	placental growth factor; vascular endothelial growth factor-related protein	Hs.2894
X60957	tyrosine kinase with immunoglobulin and epidermal growth factor homology domains	Hs.78824
X67235	hematopoietically expressed homeobox	Hs.118651
X67951	proliferation-associated gene A (natural killer-enhancing factor A)	Hs.180909

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
X69910	H.sapiens p63 mRNA for transmembrane protein	Hs.74368
X79981	cadherin 5; VE-cadherin (vascular epithelium)	Hs.76206
Z18951	caveolin 1; caveolae protein; 22kD	Hs.247266
AA187101	zp61b6.r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:624659 5', mRNA sequence	
N24990	ESTs	Hs.26418
R81003	Homo sapiens serine protease mRNA; complete cds	Hs.154737
AA025351	ESTs	Hs.134797
AA027168	ESTs	Hs.10031
AA040465	ESTs	Hs.8728
AA045136	ESTs	Hs.22575
AA054087	phospholipase A2; group IVC (cytosolic; calcium-independent)	Hs.18858
AA071089	ESTs; Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]	Hs.187932
AA085918	H.sapiens HUNKI mRNA	Hs.247482
AA187490	ESTs	Hs.21941
AA227926	ESTs	Hs.6682
AA234743	ESTs	Hs.22120
AA236559	ESTs; Weakly similar to neuronal thread protein AD7c-NTP [H.sapiens]	Hs.8768
AA292694	ESTs	Hs.3807
AA398243	ESTs; Moderately similar to (defline not available 3694664) [H.sapiens]	Hs.21806
AA406363	ESTs	Hs.30822
AA411465	ESTs	Hs.8619
AA412284	poliovirus receptor	Hs.171844
AA423987	ESTs	Hs.7567
AA425309	ESTs	Hs.33287
AA435896	ESTs	Hs.18397
AA448238	Homo sapiens mRNA for KIAA0915 protein; complete cds	Hs.16714
AA478778	ESTs	Hs.16450
AA621714	ESTs	Hs.25338
D51069	Human isolate JuSo MUC18 glycoprotein mRNA (3' variant); complete cds	Hs.211579
T34527	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1)	Hs.80120
U97519	podocalyxin-like	Hs.16426
AA127221	ESTs	Hs.71059
AA132983	ESTs; Moderately similar to C-1-TETRAHYDROFOLATE SYNTHASE; CYTOPLASMIC [H.sapiens]	Hs.44155
AA135606	ESTs; Weakly similar to !!!! ALU SUBFAMILY SB WARNING ENTRY !!!! [H.sapiens]	Hs.189384
AA156125	ESTs	Hs.72116
AA179845	RAB6 interacting; kinesin-like (rabkinesin6)	Hs.73625
AA232645	ESTs	Hs.42699
F10399	ESTs	Hs.14763
H16772	ESTs	Hs.31444
N39584	ESTs	Hs.17404

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
N52006	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1)	Hs.80120
N53375	Homer; neuronal immediate early gene; 3	Hs.166146
N54067	Homo sapiens mRNA for NIK; partial cds	Hs.3628
N64436	ESTs	Hs.20813
R26892	ESTs	Hs.221434
T33637	ESTs	Hs.6841
T57112	yc20g11.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:81284 3', mRNA sequence.	
W80763	ESTs; Moderately similar to FK506-binding protein 65kD [M.musculus]	Hs.3849
AA046808	ESTs; Highly similar to 40S RIBOSOMAL PROTEIN S27 [H.sapiens]	Hs.108957
AA253217	ESTs	Hs.41271
AA255991	ESTs	Hs.175319
AA258138	ESTs	Hs.88297
AA426573	ESTs	Hs.41135
AA443793	ESTs	Hs.94761
AA490588	ESTs	Hs.43118
AA496257	ESTs; Weakly similar to (defline not available 3513303) [H.sapiens]	Hs.72165
AA609717	ESTs; Weakly similar to MICROTUBULE-ASSOCIATED PROTEIN 1B [H.sapiens]	Hs.66048
D59570	ESTs	Hs.17132
F13787	ESTs	Hs.58596
H88157	ESTs	Hs.41105
H98988	ESTs	Hs.42612
N34287	unc5 (C.elegans homolog) C	Hs.44553
N52090	EST	Hs.47420
N66845	ESTs; Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]	Hs.165411
N68905	small inducible cytokine A5 (RANTES)	
R32894	ESTs	Hs.45514
R61715	ESTs	Hs.138237
R71234	yi54c08.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:143054 3' similar to gb|M87908|HUMALNE32 Human carcinoma cell-derived Alu RNA transcript, (rRNA); gb:S41458 ROD	
R98105	yr30g11.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:206852 3', mRNA sequence.	
T97186	small inducible cytokine A5 (RANTES)	
W80814	ESTs; Moderately similar to !!!! ALU SUBFAMILY SB WARNING ENTRY !!!! [H.sapiens]	Hs.193700
AA404418	EST	Hs.144953
AA405747	ESTs; Moderately similar to HMG-box transcription factor [M.musculus]	Hs.97865
AA488687	ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]	Hs.190307
AA599143	ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]	
AA608588	ESTs	Hs.193634

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
AA608751	ESTs; Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]	Hs.244904
C13961	EST	Hs.210115
D60302	ESTs	Hs.108977
H94892	v-ral simian leukemia viral oncogene homolog A (ras related)	Hs.6906
N93521	transcription factor 4	Hs.241362
N95477	ESTs	Hs.102943
R60044	ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]	Hs.106706
R70506	ESTs; Moderately similar to transformation-related protein [H.sapiens]	Hs.107159
T91518	ye20f05.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:118305 3' similar to contains Alu repetitive element;contains	
T95333	ESTs; Weakly similar to Strabismus [D.melanogaster]	Hs.122730
R45630	ESTs; Highly similar to KIAA0372 [H.sapiens]	Hs.170098
R20839	yg05c07.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:31444 5', mRNA sequence.	
R23858	ESTs; Moderately similar to envelope protein [H.sapiens]	Hs.23986
AI024874	ESTs; Weakly similar to (defline not available 3882257) [H.sapiens]	Hs.57958
W26247	U5 snRNP-specific protein (220 kD); ortholog of S. cerevisiae Prp8p	Hs.6413
AA856990	ESTs	Hs.125058
AA136653	ESTs	
AA358869	ESTs; Highly similar to SEC13-RELATED PROTEIN [H.sapiens]	Hs.227949
AI123976	ESTs	Hs.105689
AI369384	arylsulfatase D	
AA379500	ESTs	Hs.193155
R49693	ESTs	Hs.107708
AA195678	Homo sapiens mRNA for KIAA0465 protein; partial cds	Hs.108258
M30257	vascular cell adhesion molecule 1	Hs.109225
AA028131	ESTs	Hs.110342
M10321	Human von Willebrand factor mRNA, 3' end	Hs.110802
J03040	secreted protein; acidic; cysteine-rich (osteonectin)	Hs.111779
M86933	amelogenin (Y chromosome)	Hs.1238
AA012933	tubulin-specific chaperone d	Hs.241687
AA286710	lymphocyte adaptor protein	Hs.13131
AA243278	ribosomal protein; mitochondrial; L12	Hs.109059
D59711	ESTs	Hs.237289
T94452	ye36g7.s1 Stratagene lung (#93721) Homo sapiens cDNA clone IMAGE:119868 3', mRNA sequence	Hs.241207
AA053400	ESTs	Hs.241227
AA370302	Homo sapiens mRNA; cDNA DKFZp586I1518 (from clone DKFZp586I1518)	Hs.21739
J05008	endothelin 1	Hs.2271
U85193	nuclear factor I/B	Hs.33287
AA256153	ESTs	Hs.23912
X83107	BMX non-receptor tyrosine kinase	Hs.27372
AA046593	ESTs	Hs.28959

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
AA410480	ESTs	Hs.30089
D45304	ESTs	Hs.31595
M90657	transmembrane 4 superfamily member 1	Hs.3337
AA010163	upstream regulatory element binding protein 1	Hs.3383
AA136353	ESTs	Hs.38022
Y07867	pirin	Hs.38842
U84573	procollagen-lysine; 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2	Hs.41270
X60486	H4 histone family; member G	Hs.46423
AA132969	metalloprotease 1 (pitrilysin family)	Hs.4812
AA114250	KIAA0512 gene product	Hs.48924
F13782	LIM binding domain 2	Hs.4980
AA283035	ESTs; Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]	Hs.54813
AB002301	Human mRNA for KIAA0303 gene; partial cds	Hs.54985
AA056731	Sjogren syndrome antigen A2 (60kD; ribonucleoprotein autoantigen SS-A/Ro)	Hs.554
U68019	MAD (mothers against decapentaplegic; Drosophila) homolog 3	Hs.211578
H99198	ESTs; Moderately similar to THYMOSIN BETA-4 [H.sapiens]	Hs.56145
AA598702	bone morphogenetic protein 6	Hs.6101
N77151	Homo sapiens mRNA for KIAA0799 protein; partial cds	Hs.61638
AA505133	ESTs	Hs.62273
AB000584	prostate differentiation factor	Hs.116577
D12763	interleukin 1 receptor-like 1	Hs.66
AA253193	ESTs	Hs.6631
AA432248	ESTs	Hs.6738
AA083572	v-ral simian leukemia viral oncogene homolog A (ras related)	Hs.6906
AA479713	ESTs	Hs.71962
L40395	Homo sapiens clone 23689 mRNA; complete cds	Hs.170001
X52947	gap junction protein; alpha 1; 43kD (connexin 43)	Hs.74471
W80846	vesicle-associated membrane protein 5 (myobrevin)	Hs.74669
M34539	FK506-binding protein 1A (12kD)	Hs.752
D67029	SEC14 (S. cerevisiae)-like	Hs.75232
U09587	glycyl-tRNA synthetase	Hs.75280
M85289	Human heparan sulfate proteoglycan (HSPG2) mRNA, complete cds	Hs.211573
D10522	myristoylated alanine-rich protein kinase C substrate (MARCKS; 80K-L)	Hs.75607
W84712	calumenin	Hs.7753
D29992	tissue factor pathway inhibitor 2	Hs.78045
L34657	platelet/endothelial cell adhesion molecule (CD31 antigen)	Hs.78146
S78569	laminin; alpha 4	Hs.78672
D43636	Human mRNA for KIAA0096 gene; partial cds	Hs.79025
U97188	IGF-II mRNA-binding protein 3	Hs.79440
AA487558	ESTs	Hs.8135
M28882	Human MUC18 glycoprotein mRNA, complete cds	Hs.211579
X70683	SRY (sex determining region Y)-box 4	Hs.83484
X14787	thrombospondin 1	Hs.87409

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
AA236324	ESTs; Weakly similar to !!!! ALU CLASS A WARNING ENTRY !!!! [H.sapiens]	Hs.92381
C15324	ESTs	Hs.93668
AA452000	ESTs	Hs.94030
D83174	collagen-binding protein 2 (colligen 2)	Hs.9930
D00596	Homo sapiens gene for thymidylate synthase; exons 1; 2; 3; 4; 5; 6; 7; complete cds	Hs.196351
D11428	peripheral myelin protein 22	Hs.103724
D13640	major histocompatibility complex; class I; C	Hs.183618
D14874	adrenomedullin	Hs.394
D26129	ribonuclease; RNase A family; 1 (pancreatic)	Hs.78224
D28476	thyroid hormone receptor interactor 12	Hs.138617
D86425	Homo sapiens mRNA for nidogen-2	Hs.82733
D86983	Human mRNA for KIAA0230 gene; partial cds	Hs.118893
D87953	N-myc downstream regulated	Hs.75789
HG1862-HT1897	Calmodulin Type I	
HG2614-HT2710	Collagen, Type Viii, Alpha 1	
HG2639-HT2735	Single-Stranded Dna-Binding Protein Mssp-1	
HG2855-HT2995	Heat Shock Protein, 70 Kda (Gb:Y00371)	
HG3044-HT3742	Fibronectin, Alt. Splice 1	
HG3342-HT3519	Id1	
HG3543-HT3739	Insulin-Like Growth Factor 2	
HG4069-HT4339	Monocyte Chemotactic Protein 1	
HG417-HT417	Cathepsin B	
J03764	plasminogen activator inhibitor; type I	Hs.82085
L06797	chemokine (C-X-C motif); receptor 4 (fusin)	Hs.89414
L08246	myeloid cell leukemia sequence 1 (BCL2-related)	Hs.86386
L12711	transketolase (Wernicke-Korsakoff syndrome)	Hs.89643
L13977	prolylcarboxypeptidase (angiotensinase C)	Hs.75693
L15388	Human G protein-coupled receptor kinase (GRK5) mRNA, complete cds	
L19871	activating transcription factor 3	Hs.460
L20859	Human leukemia virus receptor 1 (GLVR1) mRNA; complete cds	Hs.78452
L42176	four and a half LIM domains 2	Hs.8302
L49169	Human G0S3 mRNA; complete cds	Hs.75678
L76380	calcitonin receptor-like	Hs.152175
M15990	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1	Hs.194148
M23254	calpain; large polypeptide L2	Hs.76288
M24736	selectin E (endothelial adhesion molecule 1)	Hs.89546
M26576	collagen; type IV; alpha 1	Hs.119129
M27396	asparagine synthetase	Hs.75692
M31166	pentaxin-related gene; rapidly induced by IL-1 beta	Hs.2050
M31994	Homo sapiens aldehyde dehydrogenase (ALDH1) gene, exon 13 and complete cds	
M32334	intercellular adhesion molecule 2	Hs.83733
M35878	insulin-like growth factor binding protein 3	Hs.77326

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
M36429	postmeiotic segregation increased 2-like 12	Hs.89672
M57730	ephrin-A1	Hs.1624
M57731	GRO2 oncogene	Hs.75765
M60858	nucleolin	Hs.79110
M62994	filamin B; beta (actin-binding protein-278)	Hs.81008
M68874	Human phosphatidylcholine 2-acylhydrolase (cPLA2) mRNA, complete cds	
M69043	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor; alpha	Hs.81328
M74719	transcription factor 4	Hs.75356
M75126	hexokinase 1	Hs.118625
M84349	CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5; EJ16; EJ30; EL32 and G344)	Hs.119663
M92843	zinc finger protein homologous to Zfp-36 in mouse	Hs.198309
M92934	connective tissue growth factor	Hs.75511
M93056	protease inhibitor 2 (anti-elastase); monocyte/neutrophil	Hs.183583
M94856	fatty acid binding protein 5 (psoriasis-associated)	Hs.153179
M95787	transgelin	Hs.75777
S76965	Protein kinase inhibitor [human; neuroblastoma cell line SH-SY-5Y; mRNA; 2147 nt]	Hs.75209
S81914	DIFFERENTIATION-DEPENDENT GENE 2	Hs.76095
U03057	singed (Drosophila)-like (sea urchin fascin homolog like)	Hs.118400
U03100	catenin (cadherin-associated protein); alpha 1 (102kD)	Hs.178452
U03877	EGF-containing fibulin-like extracellular matrix protein 1	Hs.76224
U08021	nicotinamide N-methyltransferase	Hs.76669
U14391	myosin IC	Hs.82251
U31384	guanine nucleotide binding protein 11	Hs.83381
U32944	dynein; cytoplasmic; light polypeptide	Hs.5120
U40369	Human spermidine/spermine N1-acetyltransferase (SSAT) gene, complete cds	
U41767	Human metargidin precursor mRNA, complete cds	
U48959	Homo sapiens myosin light chain kinase (MLCK) mRNA; complete cds	Hs.75950
U51010	Human nicotinamide N-methyltransferase gene, exon 1 and 5' flanking region	
U51478	ATPase; Na+/K+ transporting; beta 3 polypeptide	Hs.76941
U53445	Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA; complete cds	Hs.15432
U59289	cadherin 13; H-cadherin (heart)	Hs.63984
U59423	MAD (mothers against decapentaplegic; Drosophila) homolog 1	Hs.79067
U62015	Homo sapiens Cyr61 mRNA, complete cds	
U63825	Human hepatitis delta antigen interacting protein A (dipA) mRNA; complete cds	Hs.66713
U67963	Human lysophospholipase homolog (HU-K5) mRNA; complete cds	Hs.6721
U73379	Human cyclin-selective ubiquitin carrier protein mRNA; complete cds	Hs.93002
U73824	eukaryotic translation initiation factor 4 gamma; 2	Hs.183684
U77604	microsomal glutathione S-transferase 2	Hs.81874
U81607	kinase scaffold protein gravin	Hs.788

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
U89942	lysyl oxidase-like 2	Hs.83354
X04412	gelsolin (amyloidosis; Finnish type)	Hs.80562
X06985	heme oxygenase (decycling) 1	Hs.75967
X07820	matrix metalloproteinase 10 (stromelysin 2)	Hs.2258
X12876	keratin 18	Hs.65114
X15729	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 5 (RNA helicase; 68kD)	Hs.76053
X52541	early growth response 1	Hs.738
X53416	filamin A; alpha (actin-binding protein-280)	Hs.76279
X54489	GRO1 oncogene (melanoma growth stimulating activity; alpha)	Hs.789
X54925	matrix metalloproteinase 1 (interstitial collagenase)	Hs.83169
X57206	inositol 1;4;5-trisphosphate 3-kinase B	Hs.78877
X59798	cyclin D1 (PRAD1: parathyroid adenomatosis 1)	Hs.82932
X60957	tyrosine kinase with immunoglobulin and epidermal growth factor homology domains	Hs.78824
X65965	H.sapiens SOD-2 gene for manganese superoxide dismutase	
X69111	inhibitor of DNA binding 3; dominant negative helix-loop-helix protein	Hs.76884
X70940	eukaryotic translation elongation factor 1 alpha 2	Hs.2642
X87838	catenin (cadherin-associated protein); beta 1 (88kD)	Hs.171271
X91247	thioredoxin reductase 1	Hs.13046
X97748	H.sapiens PTX3 gene promotor region	
Y00815	protein tyrosine phosphatase; receptor type; F	Hs.75216
AA303711	ephrin-B1	Hs.144700
L44538	ESTs	Hs.156044
AA025351	ESTs	Hs.134797
AA027050	ESTs	Hs.31189
AA029462	ESTs	Hs.17235
AA045136	ESTs	Hs.22575
AA047437	ESTs	Hs.22968
AA054087	phospholipase A2; group IVC (cytosolic; calcium-independent)	Hs.18858
AA071089	ESTs; Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]	Hs.187932
AA156450	ESTs; Weakly similar to Similar to Rat trg gene product [C.elegans]	Hs.8982
AA187490	ESTs	Hs.21941
AA195031	ESTs; Moderately similar to PROBABLE G PROTEIN-COUPLED RECEPTOR APJ [H.sapiens]	Hs.9305
AA205724	ESTs	Hs.10119
AA227926	ESTs	Hs.6682
AA227986	ESTs	Hs.25329
AA234743	ESTs	Hs.22120
AA253216	ESTs	Hs.22283
AA256210	oncomodulin	Hs.199134
AA256268	ESTs	Hs.10283
AA279397	ESTs; Moderately similar to fibronectin [H.sapiens]	Hs.25001
AA292379	ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]	Hs.20340

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
AA292717	ESTs; Weakly similar to JM2 [H.sapiens]	Hs.7891
AA346551	ESTs	Hs.23457
AA400292	ESTs	Hs.23786
AA404338	ESTs	Hs.21812
AA412284	poliovirus receptor	Hs.171844
AA423987	ESTs	Hs.7567
AA428594	ESTs	Hs.21321
AA430108	ESTs	Hs.6019
AA431462	ESTs	Hs.28329
AA431470	ESTs; Weakly similar to CAMP-DEPENDENT PROTEIN KINASE INHIBITOR; MUSCLE/BRAIN FORM [H.sapiens]	Hs.3407
AA443756	ESTs; Moderately similar to (defline not available 4105275) [H.sapiens]	Hs.6673
AA449479	ESTs; Highly similar to (defline not available 5106787) [H.sapiens]	Hs.5216
AA459916	bradykinin receptor B2	Hs.25021
AA465226	ESTs	Hs.28631
AA478778	ESTs	Hs.16450
AA479037	ESTs	Hs.7961
AA482597	ESTs; Highly similar to (defline not available 4704739) [H.sapiens]	Hs.26054
AA487561	ESTs; Highly similar to RAS-RELATED PROTEIN RAB-1A [H.sapiens]	Hs.9813
AA489245	ESTs; Weakly similar to sperm specific protein [H.sapiens]	Hs.5682
AA504110	ESTs	Hs.18063
AA520989	ESTs; Highly similar to SERINE/THREONINE PROTEIN PHOSPHATASE PP1-BETA CATALYTIC SUBUNIT [H.sapiens]	Hs.9195
AA599434	ESTs	Hs.25035
AA608649	Homo sapiens clone 23742 mRNA; partial cds	Hs.6354
AA609519	ESTs	Hs.26458
D51069	Human isolate JuSo MUC18 glycoprotein mRNA (3' variant); complete cds	Hs.185718
U97519	podocalyxin-like	Hs.16426
W28391	proliferation-associated 2G4; 38kD	Hs.5181
AA035638	Homo sapiens mRNA; cDNA DKFZp564F053 (from clone DKFZp564F053)	Hs.71968
AA083514	ESTs	Hs.68301
AA121315	ESTs	Hs.70823
AA147186	ESTs	Hs.92387
AA156125	ESTs	Hs.72116
AA188932	ESTs	Hs.85640
AA219653	ESTs	Hs.87125
AA232645	ESTs	Hs.42699
F10078	ESTs	Hs.13233
H48032	ESTs	Hs.9645
H82117	ESTs	Hs.28043
N39584	ESTs	Hs.17404
N54067	Homo sapiens mRNA for NIK; partial cds	Hs.3628
N59858	ESTs	Hs.33032

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
N90933	ESTs	Hs.4867
N93764	ESTs; Moderately similar to !!!! ALU CLASS C WARNING ENTRY !!!! [H.sapiens]	Hs.10175
R26124	ESTs	Hs.24024
R27957	ESTs	Hs.24230
R55470	ESTs; Moderately similar to K02E10.2 [C.elegans]	Hs.11067
T16550	ESTs; Highly similar to vacuolar protein sorting homolog h-vps45 [H.sapiens]	Hs.6650
T26674	ESTs; Weakly similar to neuronal thread protein AD7c-NTP [H.sapiens]	Hs.6966
T57112	yc20g11.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:81284 3', mRNA sequence.	Hs.8881
T88700	ESTs	Hs.173374
T90527	ESTs	Hs.7890
W42789	ESTs	Hs.31446
W60002	plastin 3 (T isoform)	Hs.4114
W78175	ESTs	Hs.17901
W84768	ESTs	Hs.141742
W94427	ESTs; Weakly similar to Na;K-ATPase gamma subunit [H.sapiens]	Hs.3807
AA253217	ESTs	Hs.41271
AA426573	ESTs	Hs.41135
AA432374	ESTs	Hs.48029
AA446622	ESTs	Hs.74313
AA478771	ESTs	Hs.50841
AA482594	ESTs	Hs.62684
AA490588	ESTs	Hs.43118
D59570	ESTs	Hs.17132
H88157	ESTs	Hs.41105
H94648	ESTs	Hs.41995
H97538	ESTs	Hs.42392
H98670	ESTs; Weakly similar to (defline not available 4884081) [H.sapiens]	Hs.49753
N22107	ESTs; Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]	Hs.172241
W38197	Accession not listed in Genbank	
W80814	ESTs; Moderately similar to !!!! ALU SUBFAMILY SB WARNING ENTRY !!!! [H.sapiens]	Hs.196785
AA287347	ESTs	Hs.105088
AA402799	ESTs	Hs.182538
AA404418	EST	Hs.144953
AA425107	ESTs	Hs.97016
AA425435	ESTs; Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]	Hs.98438
AA442872	ESTs	Hs.110771
AA452860	ESTs; Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]	Hs.197214
AA488687	ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]	Hs.190307
AA599674	ESTs; Weakly similar to ORF [D.melanogaster]	Hs.108115

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
F13673	ESTs	Hs.99769
H99093	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide (72kD)	Hs.6179
N22495	yw35g11.s1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:254276 3', mRNA sequence.	Hs.102415
N23031	myosin; heavy polypeptide 7; cardiac muscle; beta	Hs.929
R15740	carbohydrate (chondroitin 6/keratan) sulfotransferase 1	Hs.104576
R39610	calpain; large polypeptide L2	Hs.76288
W45560	ESTs	Hs.102541
Z39833	H.sapiens mRNA for Rho6 protein	Hs.124940
Z40583	ESTs	Hs.101259
AA825437	ESTs	
R66613	Homo sapiens mRNA; cDNA DKFZp564F053 (from clone DKFZp564F053)	
AA868063	carbohydrate (chondroitin 6/keratan) sulfotransferase 1	
AA128075	zl16d08.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:502095 5', mRNA sequence.	
N66570	ESTs	
AI051390	ESTs	
AA627122	ESTs	
X02761	fibronectin 1	Hs.118162
AF010193	MAD (mothers against decapentaplegic; Drosophila) homolog 7	Hs.100602
AA149044	ESTs; Highly similar to the KIAA0195 gene is expressed ubiquitously. [H.sapiens]	Hs.10086
U82108	solute carrier family 9 (sodium/hydrogen exchanger); isoform 3 regulatory factor 2	Hs.101813
D78676	ESTs; Moderately similar to (defline not available 4529890) [H.sapiens]	Hs.105509
L35240	enigma (LIM domain protein)	Hs.102948
AA598737	lactate dehydrogenase B	Hs.180414
R69417	ESTs	Hs.107055
AA232837	ESTs; Weakly similar to Human pre-mRNA cleavage factor I 68 kDa subunit [H.sapiens]	Hs.107125
N72695	ESTs	Hs.108557
M30257	vascular cell adhesion molecule 1	Hs.109225
M96843	inhibitor of DNA binding 2; dominant negative helix-loop-helix protein	Hs.109617
X68277	dual specificity phosphatase 1	Hs.171695
AA292440	myeloid differentiation primary response	Hs.110571
J03040	secreted protein; acidic; cysteine-rich (osteonectin)	Hs.111779
AA228107	ESTs	Hs.54642
AA449789	connective tissue growth factor	Hs.75511
W01367	ESTs	Hs.170980
AA610116	ESTs; Highly similar to (defline not available 4325180) [H.sapiens]	Hs.11663
AA258308	Homo sapiens mRNA; cDNA DKFZp564F053 (from clone DKFZp564F053)	Hs.165618
AA460273	Homo sapiens mRNA for KIAA0517 protein; partial cds	Hs.12372
AA286710	lymphocyte adaptor protein	Hs.13131
T68873	metallothionein 1L	Hs.143289

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
D63476	PAK-interacting exchange factor beta	Hs.172813
M62403	insulin-like growth factor-binding protein 4	Hs.1516
X55740	5' nucleotidase (CD73)	Hs.153952
L10284	calnexin	Hs.155560
AA243278	ribosomal protein; mitochondrial; L12	Hs.109059
AA430032	pituitary tumor-transforming 1	Hs.159626
H16402	ESTs	Hs.17121
D59711	ESTs	Hs.17132
T94452	ye36g7.s1 Stratagene lung (#93721) Homo sapiens cDNA clone IMAGE:119868 3', mRNA sequence	
AA431571	ESTs	Hs.17894
R79356	Homo sapiens mRNA for KIAA0544 protein; partial cds	Hs.19280
AA280375	ESTs	Hs.19928
Z49269	small inducible cytokine subfamily A (Cys-Cys); member 14	Hs.20144
Z41740	ESTs	Hs.24462
AA121543	Homo sapiens mRNA for KIAA0758 protein; partial cds	Hs.22039
J05008	endothelin 1	Hs.2271
AA101878	ESTs	Hs.22793
T35341	ESTs; Highly similar to (defline not available 4519883) [H.sapiens]	Hs.22880
N87590	ESTs	Hs.23037
AA256153	ESTs	Hs.23912
W74533	Homo sapiens mRNA for KIAA0786 protein; partial cds	Hs.24212
U25997	stanniocalcin	Hs.25590
V01512	v-fos FBJ murine osteosarcoma viral oncogene homolog	Hs.25647
X56681	jun D proto-oncogene	Hs.2780
AA161292	interferon; alpha-inducible protein 27	Hs.2867
AA491465	ESTs	Hs.28792
AA046593	ESTs	Hs.28959
D50914	Human mRNA for KIAA0124 gene; partial cds	Hs.30736
D45304	ESTs	Hs.31595
M90657	transmembrane 4 superfamily member 1	Hs.3337
W69127	ESTs; Weakly similar to zinc finger protein ZNF191 [H.sapiens]	Hs.3449
AA316186	ESTs; Highly similar to (defline not available 4262136) [H.sapiens]	Hs.34549
AA384503	ESTs	Hs.179260
AA136353	ESTs	Hs.38022
AA044755	ESTs; Weakly similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]	Hs.173705
U84573	procollagen-lysine; 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2	Hs.41270
AA058911	ESTs; Weakly similar to membrane glycoprotein [M.musculus]	Hs.4193
AA620962	dynein; cytoplasmic; light intermediate polypeptide 2	Hs.44251
AA285290	small EDRK-rich factor 2	Hs.44499
X60486	H4 histone family; member G	Hs.46423
R31641	ESTs	Hs.197148
AA489190	ESTs	Hs.48320
F13782	LIM binding domain 2	Hs.4980

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
AA257993	Janus kinase 1 (a protein tyrosine kinase)	Hs.50651
M24283	intercellular adhesion molecule 1 (CD54); human rhinovirus receptor	Hs.168383
AA443114	ESTs; Weakly similar to PIM-1 PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE [H.sapiens]	Hs.5326
T35289	casein kinase 1; alpha 1	Hs.195206
N23817	Homo sapiens clone 23675 mRNA sequence	Hs.5807
AA047151	ESTs	Hs.5897
N77151	Homo sapiens mRNA for KIAA0799 protein; partial cds	Hs.61638
AA480074	ESTs	Hs.62206
Y00787	interleukin 8	Hs.624
T99789	ESTs	Hs.64313
W84341	tissue inhibitor of metalloproteinase 2	Hs.6441
L09209	amyloid beta (A4) precursor-like protein 2	Hs.64797
D12763	interleukin 1 receptor-like 1	Hs.66
T16484	ESTs	Hs.6607
AA253193	ESTs	Hs.6631
AA432248	ESTs	Hs.6738
X82200	stimulated trans-acting factor (50 kDa)	Hs.68054
AA083572	v-ral simian leukemia viral oncogene homolog A (ras related)	Hs.6906
L00352	low density lipoprotein receptor (familial hypercholesterolemia)	Hs.181182
N75791	ESTs	Hs.7153
X57579	H.sapiens activin beta-A subunit (exon 2)	
X02612	cytochrome P450; subfamily I (aromatic compound-inducible); polypeptide 1	Hs.72912
H44631	immediate early protein	Hs.737
AA090257	superoxide dismutase 2; mitochondrial	Hs.177781
X83703	H.sapiens mRNA for cytokine inducible nuclear protein	Hs.74019
L40395	Homo sapiens clone 23689 mRNA; complete cds	Hs.170001
AA227913	ESTs	Hs.198456
X52947	gap junction protein; alpha 1; 43kD (connexin 43)	Hs.74471
M11313	alpha-2-macroglobulin	Hs.74561
L14837	tight junction protein 1 (zona occludens 1)	Hs.74614
M60721	Human homeobox gene, complete cds	
D90209	activating transcription factor 4 (tax-responsive enhancer element B67)	Hs.181243
T67986	yc28e12.s1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:82030 3' similar to gb:X14723 CLUSTERIN PRECURSOR	Hs.75106
AA148318	Human mRNA for KIAA0069 gene; partial cds	Hs.75249
U97105	dihydropyrimidinase-like 2	Hs.173381
T25747	H.sapiens OZF mRNA	Hs.75471
K02574	Accession not listed in Genbank	
D78577	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein; eta polypeptide	Hs.75544
X53331	matrix Gla protein	Hs.75742
S73591	upregulated by 1;25-dihydroxyvitamin D-3	Hs.179526
X95735	zyxin	Hs.75873

Exemplar Accession	Complete Title	UniGeneID(11/29/99)
L16862	G protein-coupled receptor kinase 6	Hs.76297
U44975	Homo sapiens Kruppel-like zinc finger protein Zf9 mRNA; complete cds	Hs.76526
M97796	inhibitor of DNA binding 2; dominant negative helix-loop-helix protein	Hs.180919
U86782	26S proteasome-associated pad1 homolog	Hs.178761
AA099391	ESTs	Hs.77310
M19267	tropomyosin 1 (alpha)	Hs.77899
D29992	tissue factor pathway inhibitor 2	Hs.78045
L19314	phosphorylase kinase; beta	Hs.195217
S78569	laminin; alpha 4	Hs.78672
U28811	Human cysteine-rich fibroblast growth factor receptor (CFR-1) mRNA, complete cds	
L77886	protein tyrosine phosphatase; receptor type; K	Hs.79005
C14407	neuronal tissue-enriched acidic protein	Hs.79516
M60278	diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor)	Hs.799
R81509	splicing factor; arginine/serine-rich 11	Hs.184571
AA487558	ESTs	Hs.8135
D86962	KIAA0207 gene product	Hs.81875
AA478971	disabled (Drosophila) homolog 2 (mitogen-responsive phosphoprotein)	Hs.81988
D50683	transforming growth factor; beta receptor II (70-80kD)	Hs.82028
U56637	capping protein (actin filament) muscle Z-line; alpha 1	Hs.184270
M61199	Human cleavage signal 1 protein mRNA; complete cds	Hs.82767
M28882	Human MUC18 glycoprotein mRNA, complete cds	
X15183	CDW52 antigen (CAMPATH-1 antigen)	Hs.180532
S53911	CD34	Hs.85289
U20734	Human transcription factor junB (junB) gene; 5' region and complete cds	Hs.198951
D28235	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	Hs.92309
AA236324	ESTs; Weakly similar to !!!! ALU CLASS A WARNING ENTRY !!!! [H.sapiens]	Hs.92381
AA148923	Homo sapiens mRNA for DEPP (decidual protein induced by progesterone); complete cds	Hs.93675
AA174183	ESTs	Hs.93872
AA456311	ESTs; Weakly similar to !!!! ALU CLASS A WARNING ENTRY !!!! [H.sapiens]	Hs.93961
L08069	heat shock protein; DNAJ-like 2	Hs.94
AA452000	ESTs	Hs.94030
AA282140	ESTs	Hs.9587
J02854	myosin regulatory light chain 2; smooth muscle isoform	Hs.9615
AA442054	phospholipase C; gamma 1 (formerly subtype 148)	Hs.993

TABLE 5

Accession #	UniGeneID	Title	Gene	Eos #
AA426573	Hs.41135	ESTs; Moderately similar to endomucin [M.musculus]		AAA9
D58024	Hs.57958	ESTs; Weakly similar to KIAA0768 protein [H.sapiens]		AAA8
M31210	Hs.154210	endothelial differentiation; sphingolipid G-protein-coupled receptor; 1	EDG1	AAA7
X06256	Hs.149609	integrin; alpha 5 (fibronectin receptor; alpha polypeptide)	ITGA5	AAB1
L20859	Hs.78452	solute carrier family 20 (phosphate transporter); member 1	SLC20A1	AAB3
X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin 2)	MMP10	AAB4
AA234743	Hs.22120	ESTs		AAB5
U97519	Hs.16426	podocalyxin-like	PODXL	AAB6
U03877	Hs.76224	EGF-containing fibulin-like extracellular matrix protein 1	EFEMP1	AAB8
M28882	Hs.211579	melanoma adhesion molecule	MCAM	AAB9
X54925	Hs.83169	matrix metalloproteinase 1 (interstitial collagenase)	MMP1	AAC1
AA045136	Hs.22575	ESTs		AAC2
AA423987	Hs.7567	ESTs		AAC3
AA234743	Hs.22120	ESTs		AAC4
AA156125	Hs.72116	ESTs; Moderately similar to hedgehog-interacting protein [M.musculus]		AAC5
AA025351	Hs.134797	ESTs		AAC6
AA432248	Hs.6738	ESTs		AAC7
AA227926	Hs.6682	ESTs		AAC8
AA187490	Hs.21941	ESTs		AAD1
AA232645	Hs.42699	ESTs		AAD2

CLAIMS

We claim:

1. A method of screening drug candidates comprising:

a) providing a cell that expresses an expression profile gene which encodes a protein selected from the group consisting of a nucleic acid of Table 1, Table 2, Table 3, Table 4 and Table 5 or a fragment thereof;

b) adding a drug candidate to said cell; and

c) determining the effect of said drug candidate on the expression of said expression profile gene.

2. A method according to claim 1 wherein said determining comprises comparing the level of expression in the absence of said drug candidate to the level of expression in the presence of said drug candidate, wherein the concentration of said drug candidate can vary when present, and wherein said comparison can occur after addition or removal of the drug candidate.

3. A method according to claim 1 wherein the expression of said profile gene is decreased as a result of the introduction of the drug candidate.

4. A method of screening for a bioactive agent capable of binding to a angiogenesis modulator protein (AMP), wherein said AMP is encoded by a nucleic acid selected from the group consisting of a nucleic acid of Table 1, Table 2, Table 3, Table 4 and Table 5, or a fragment thereof, said method comprising combining said AMP and a candidate bioactive agent, and determining the binding of said candidate agent to said AMP.

5. A method for screening for a bioactive agent capable of modulating the activity of a angiogenesis modulator protein (AMP), wherein said AMP is encoded by a nucleic acid selected from the group consisting of a nucleic acid of Table 1, Table 2, Table 3, Table 4 and Table 5, or a fragment thereof, said method comprising:

a) combining said AMP and a candidate bioactive agent; and

b) determining the effect of said candidate agent on the bioactivity of said AMP.

6. A method of evaluating the effect of a candidate angiogenesis drug comprising:

a) administering said drug to a patient;

b) removing a cell sample from said patient; and

c) determining the expression profile of said cell.

7. A method according to claim 6 further comprising comparing said expression profile to an expression profile of a healthy individual.

8. A method of diagnosing angiogenesis comprising:

a) determining the expression of one or more genes selected from the group consisting of a nucleic acid of Table 1, Table 2, Table 3, Table 4 and Table 5, or a fragment thereof in a first tyupe of a first individual; and

b) comparing said expression of said gene(s) from a second normal tissue type from said first individual or a second unaffected individual, wherein a difference in said expression indicates that the first individual has tissue that is undergoing angiogenesis.

9. A biochip comprising a nucleic acid segment selected from the group consisting of the sequences set forth in Table 1, Table 2, Table 3, Table 4 and Table 5, wherein said biochip comprises fewer than 1000 nucleic acid probes.

10. A biochip according to claim 9 comprising at least two nucleic acid segments.

11. A method for screening for a bioactive agent capable of interfering with the binding of an angiogenesis modulator protein (AMP) or a fragment thereof and an antibody which binds to said AMP or fragment thereof, said method comprising:

a) combining anAMP or fragment thereof, a candidate bioactive agent and an antibody which binds to said AMP or fragment thereof; and

b) determining the binding of said AMP or fragment thereof and said antibody.

12. A method for inhibiting the activity of an angiogenesis modulator protein (AMP), wherein said AMP is encoded by a nucleic acid selected from the group consisting of a nucleic acid of Table 1, Table 2, Table 3, Table 4 and Table 5 or a fragment thereof, said method comprising binding an inhibitor to said AMP.

13. A method according to claim 12 wherein said inhibitor is an antibody.

14. A method of treating a disorder associated with angiogenesis comprising administering to a patient an inhibitor of n angiogenesis modulator protein (AMP), wherein said AMP is encoded by a nucleic acid selected from the group consisting of a nucleic acid of Table 1, Table 2, Table 3, Table 4 and Table 5 or a fragment thereof.

15. A method according to claim 14 wherein said inhibitor is an antibody.

16. A method of neutralizing the effect of an AMP, or a fragment thereof, comprising contacting an agent specific for said protein with said protein in an amount sufficient to effect neutralization.

17. A method for localizing a therapeutic moiety to angioggenic tissue comprising exposing said tissue to an antibody to an AMP or fragment thereof conjugated to said therapeutic moiety.

18. The method of Claim 17, wherein said therapeutic moiety is a cytotoxic agent.

19. The method of Claim 17, wherein said therapeutic moiety is a radioisotope.

20. A method for inhibiting angiogenesis in a cell, wherein said method comprises administering to a cell a composition comprising antisense molecules to a nucleic acid of Table 1, Table 2, Table 3, Table 4 or Table 5.

21. An antibody which specifically binds to a protein encoded by a nucleic acid of Table 1, Table 2, Table 3, Table 4 or Table 5 or a fragment thereof.

22. The antibody of Claim 21, wherein said antibody is a monoclonal antibody.

23. The antibody of Claim 21, wherein said antibody is a humanized antibody.

24. The antibody of Claim 21, wherein said antibody is an antibody fragment.

25. A nucleic acid having a sequence at least 95% homologous to a sequence of a nucleic acid of Table 1, Table 2, Table 3, Table 4 or Table 5 or its complement.

26. A nucleic acid which hybridizes under high stringency to a nucleic acid of Table 1, Table 2, Table 3, Table 4 or Table 5 or its complement.

27. A polypeptide encoded by the nucleic acid of Claim 25 or 26.

28. A method of eliciting an immune response in an individual, said method comprising administering to said individual a composition comprising the polypeptide of Claim 27 or a fragment thereof.

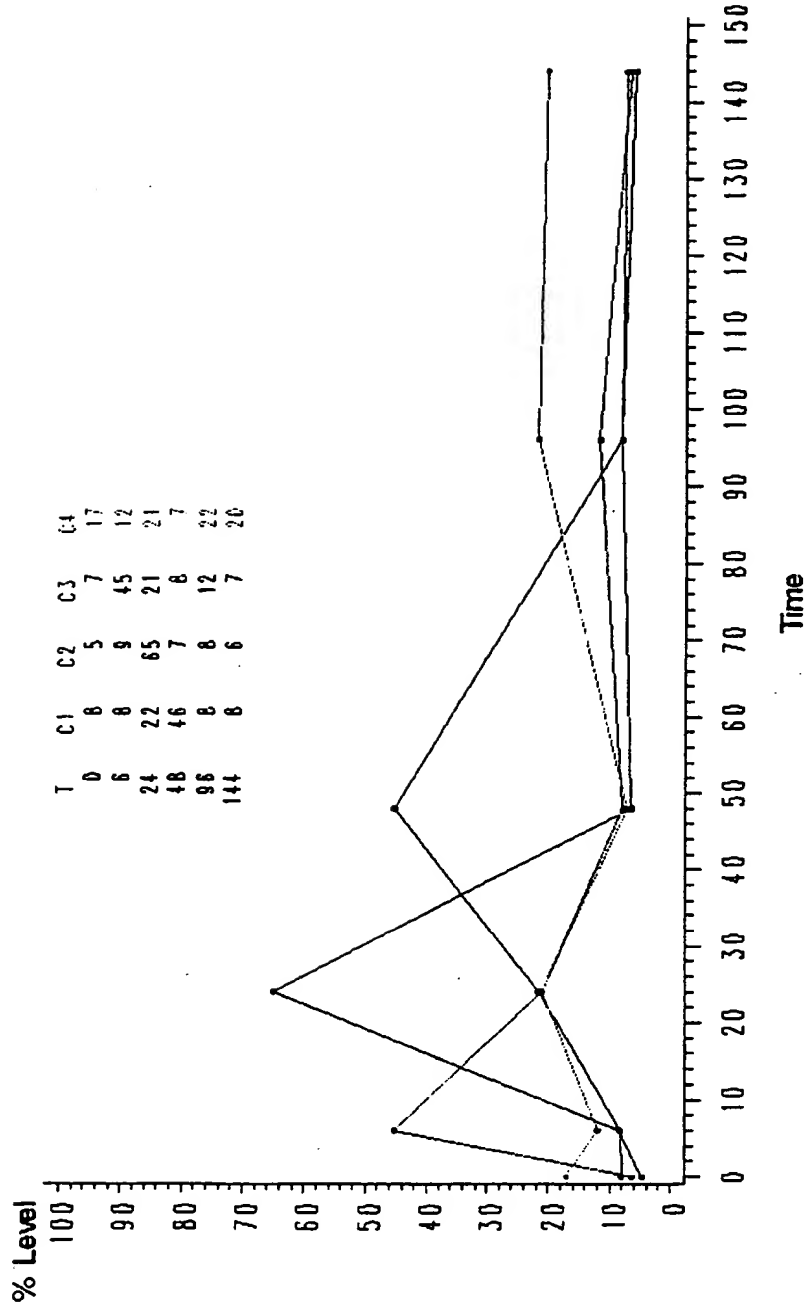
29. A method of eliciting an immune response in an individual, said method comprising administering to said individual a composition comprising a nucleic acid comprising a sequence of a nucleic acid of Table 1, Table 2, Table 3, Table 4 or Table 5 or a fragment thereof.

30. A method for determining the prognosis of an individual with a disorder associated with angiogenesis comprising determining the level of a AMP in a sample, wherein a high level of the AMP indicates a poor prognosis.

31. A method of treating a disorder associated with angiogenisis comprising administering to an individual having a disorder associated with angiogenesis an antibody to a AMP or fragment thereof conjugated to a therapeutic moiety.

32. The method of Claim 31, wherein said therapeutic moiety is a cytotoxic agent.

33. The method of Claim 31, wherein said therapeutic moiety is a radioisotope.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T C1 C2 C3 C4
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80
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20
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0
0 10 20 30 40 50 60 70 80 90 100 110 120 130 140 150
Time

FIGURE 1

FIGURE 2

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TGAAGGCCTCGCTGGAGATCGAGTACCAAGTTTTAGATGGAGCAGGATTAGATATTGATTTCCATCTTGCCTCTCCAGAA
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AACAGCATCAAGTCCAGACTAAGCAAAAGTGGGCACATACAAACTCTGCTTAGAGCATTTGAAGCTCGTGATCGAAACAT
ACAAGAAAGCAACTTTGATAGAGTCAATTTCTGGTCTATGGTTAATTTAGTGGTCATGGTGGTGGTGTCAGCCATTCAAG
TTTATATGCTGAAGAGTCTGTTTGAAGATAAGAGGAAAAGTAGAACTTAA

FIGURE 3

FIGURE 4

MGDKIWLPFPVLLLAALPPVLLPGAAGFTPSLDSDFTFTLPAGQKECFYQPMPLKASLEIEYQVLDGAGL
DIDFHLASPEGRTLVFEQRKSDGVHTVETEVGDYMFCFDNTFSTISEKVIFFELILDNMGEQAQEQEDWK
KYITGTDILDMKLEDILESINSIKSRLSKSGHIQTLLRAFEARDRNIQESNFDRVNFWSMVNLVVMVVVS
ATQVYMLKSLFEDKRKSRT.

FIGURE 5

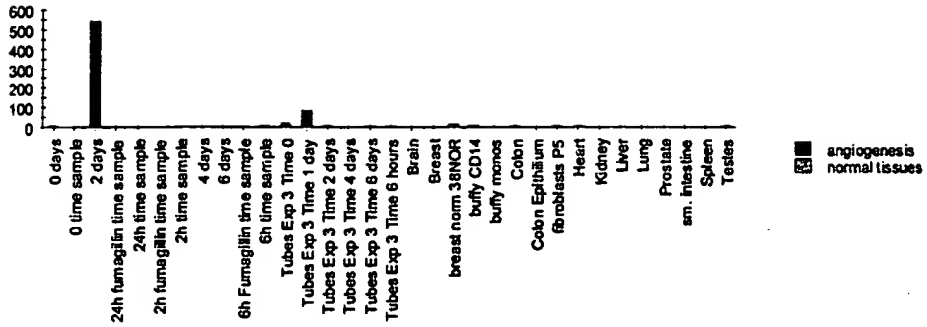
Peptide Name: AAA4p1

Sequence: H-Cys-Met-Leu-Lys-Ser-Leu-Phe-Glu-Asp-Lys
-Arg-Lys-Ser-Arg-Thr-OH

Peptide Name: AAA4p2

Sequence: H-Cys-Ala-Gly-Phe-Thr-Pro-Ser-Leu-Asp-Ser-Asp
-Phe-Thr-Phe-Thr-NH_2

FIGURE 6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Colon
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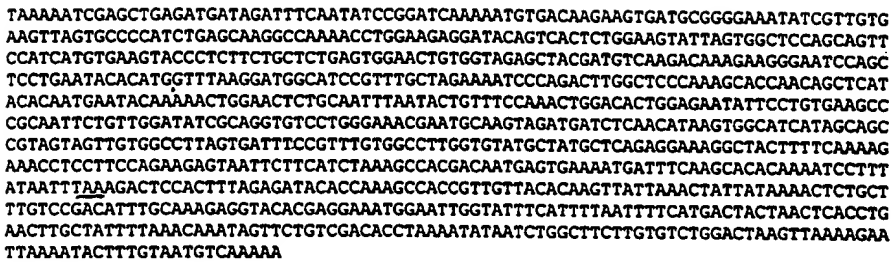
Spleen
Testes
angiogenesis
normal tissues

FIGURE 7



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TTGTCCGACATTTGCAAAGAGGTACACGAGGAAATGGAATTGGTATTTCATTTTAATTTTCATGACTACTAACTCACCTG
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TTAAAATACTTTGTAATGTCAAAAA

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VVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENDFKHTKSFII.

FIGURE 8

FIGURE 9

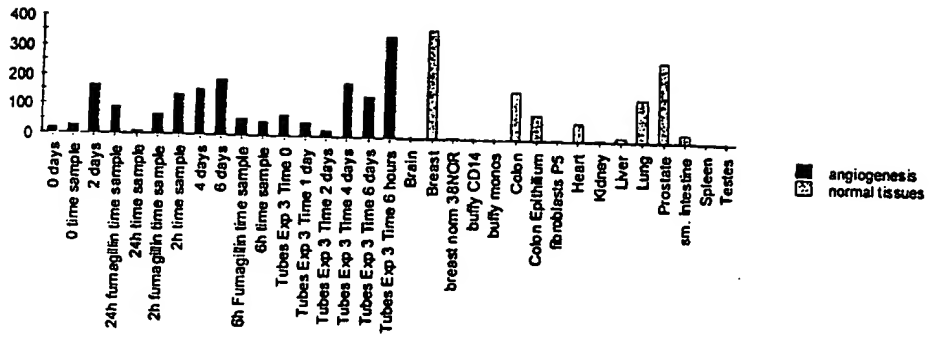
Peptide Name: AAA1p1

Sequence: H-Cys-Ala-Thr-Thr-Met-Ser-Glu-Asn-Asp-Phe-Lys-His-Thr-Lys-Ser-NH_2

Peptide Name: AAA1p2

Sequence: Ac-Arg-Cys-Gln-Asp-Lys-Glu-Gly-Asn-Pro-Ala-Pro-Glu-Tyr-Thr-NH_2

FIGURE 10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Lung
Prostate
sm. Intestine
Spleen
Testes
angiogenesis
normal tissues

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TCATTTTGCACATAGCTTTATCAACTTTTAAACATTAATAAACTGATTTTTTTAAAG

FIGURE 11

FIGURE 12

ATGGGGCCCACCAGCGTCCCGCTGGTCAAGGCCCACCGCAGCTCGGTCTCTGACTACGTCAACTATGATATCATCGTCCG
GCATTACAACTACACGGGAAAGCTGAATATCAGCGCGGACAAGGAGAACAGCATTAAACTGACCTCGGTGGTGTTCATTC
TCATCTGCTGCTTTATCATCCTGGAGAACATCTTTGTCTTGCTGACCATTTGGAAAACCAAGAAATTCCACCGACCCATG
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CACCACCTACAAGCTCACTCCCGCCCAGTGGTTTCTGCGGGAAGGGAGTATGTTTGTGGCCCTGTCAGCCTCCGTGTTCA
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CTGGAAACGTCAACTCTTCTTCCTAG

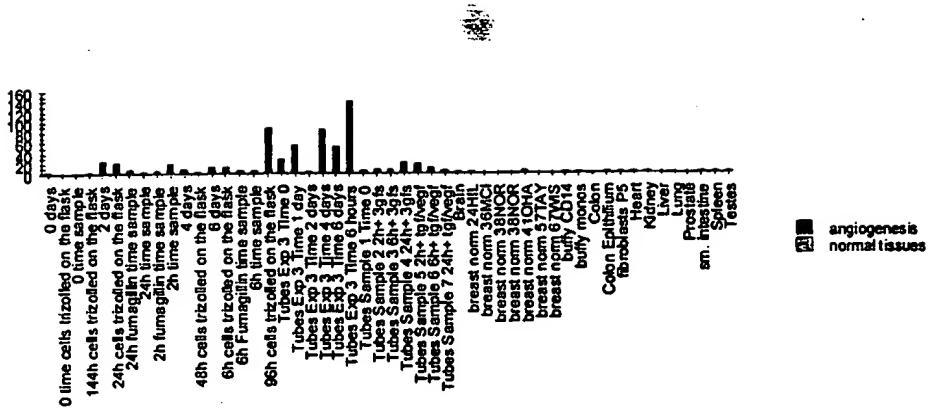
FIGURE 13

MGPTSVPLVKAHRSSVSDYVNYDIIVRHYNYTGKLNISADKENSIKLTSVVFILICCFIILENIFVLLTIWKTKKFHRPM
YYFIGNLALSDLLAGVAYTANLLLSGATTYKLTPAQWFLREGSMFVALSASVFSLLAIAIERYITMLKMKLHNGSNNFRL
FLLISACWVISLILGGLPIMGWNCISALSSCSTVLPLYHKHYILFCTTVFTLLLLSIVILYCRIYSLVRTRSRRLTFRKN
ISKASRSSENVALLKTVIIVLSVFIACWAPLFILLLLDVGCKVKTCDILFRAEYFLVLAVLNSGTNPIIYTLTNKEMRRA
FIRIMSCCKCPSGDSAGKFKRPIIAGMEFSRSKSDNSSHPQKDEGDNPETIMSSGNVNSSS.

FIGURE 14

Peptide names	amino acid sequence	Solubility
AAA7p1	Ac-KLNISADKENSIKLC-NH2	1mg/1ml H2O
AAA7p2	H-CTTYKLTPAQWFLRE-NH2	min.amt.DMSO/H2O
AAA7p3	H-CNPIIYTLTNKEMRR-NH2	1mg/1ml H2O
AAA7p1m	Ac-KLNIGAEKDHGIKLC-NH2	1mg/1ml H2O

FIGURE 15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0 time sample
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24h fumagillin time sample
24h time sample
2h fumagillin time sample
2h time sample
4 days
48h cells trizolled on the flask
8 days
6h cells trizolled on the flask
6h Fumagillin time sample
6h time sample
96h cells trizolled on the flask
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Tubes Exp 3 Time 2 days
Tubes Exp 3 Time 4 days
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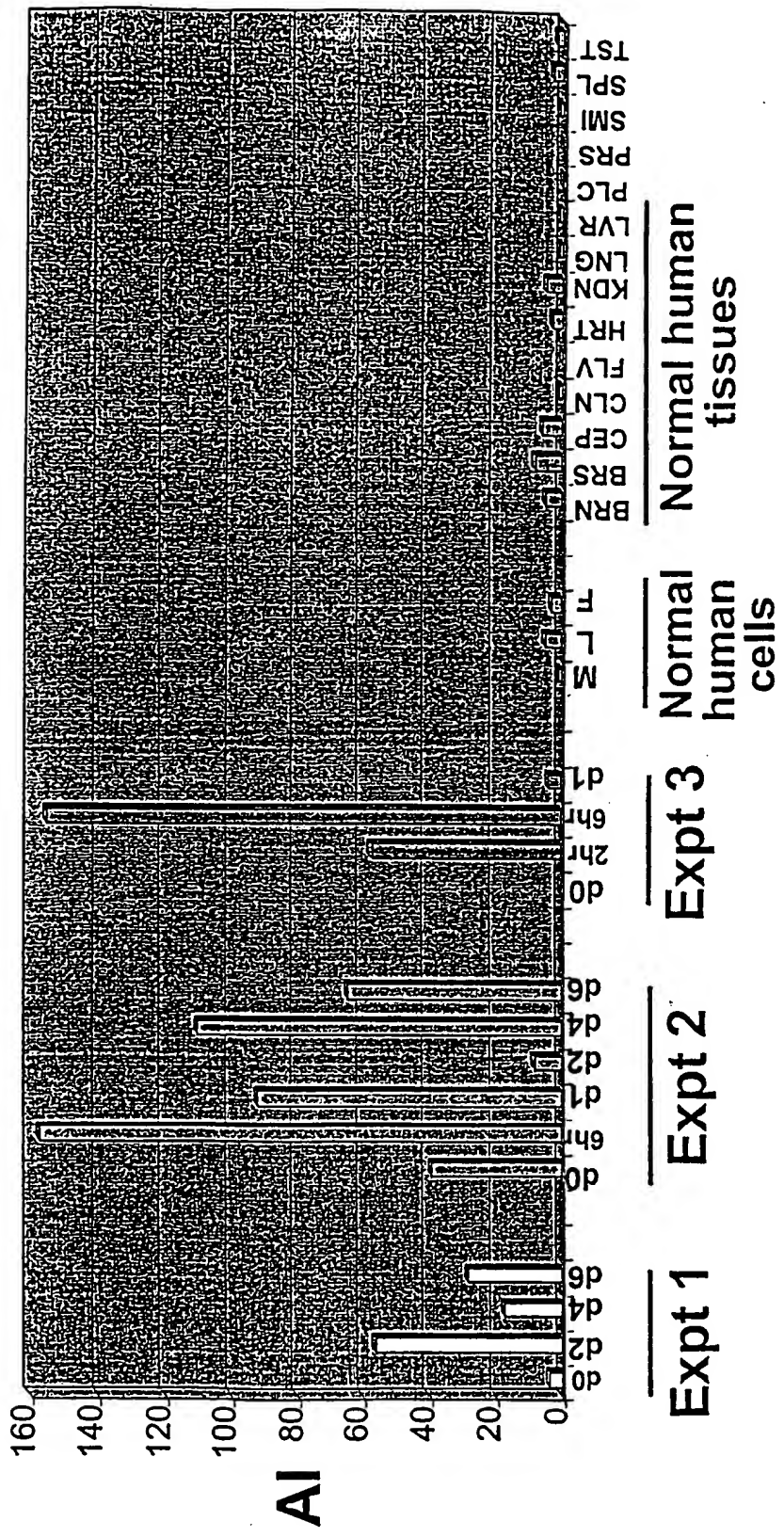
Tubes Sample 7 24h+ tg/Vegf
Brain
breast norm 24HIL
breast norm 35MICH
breast norm 38NOR
breast norm 38NOR
breast norm 41DAV
breast norm 57YAS
breast norm 57YAS
bulk CD14
buffy mono
Colon
Colon Epithelium
fibroblasts P5
Heart
Kidney
Liver
Lung
Prostate
sm. Intestine
Spleen
Testes
angiogenesis
normal tissues

FIGURE 16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M
L
F
Normal human tissues
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PLC
PRS
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SPL
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FIGURE 17

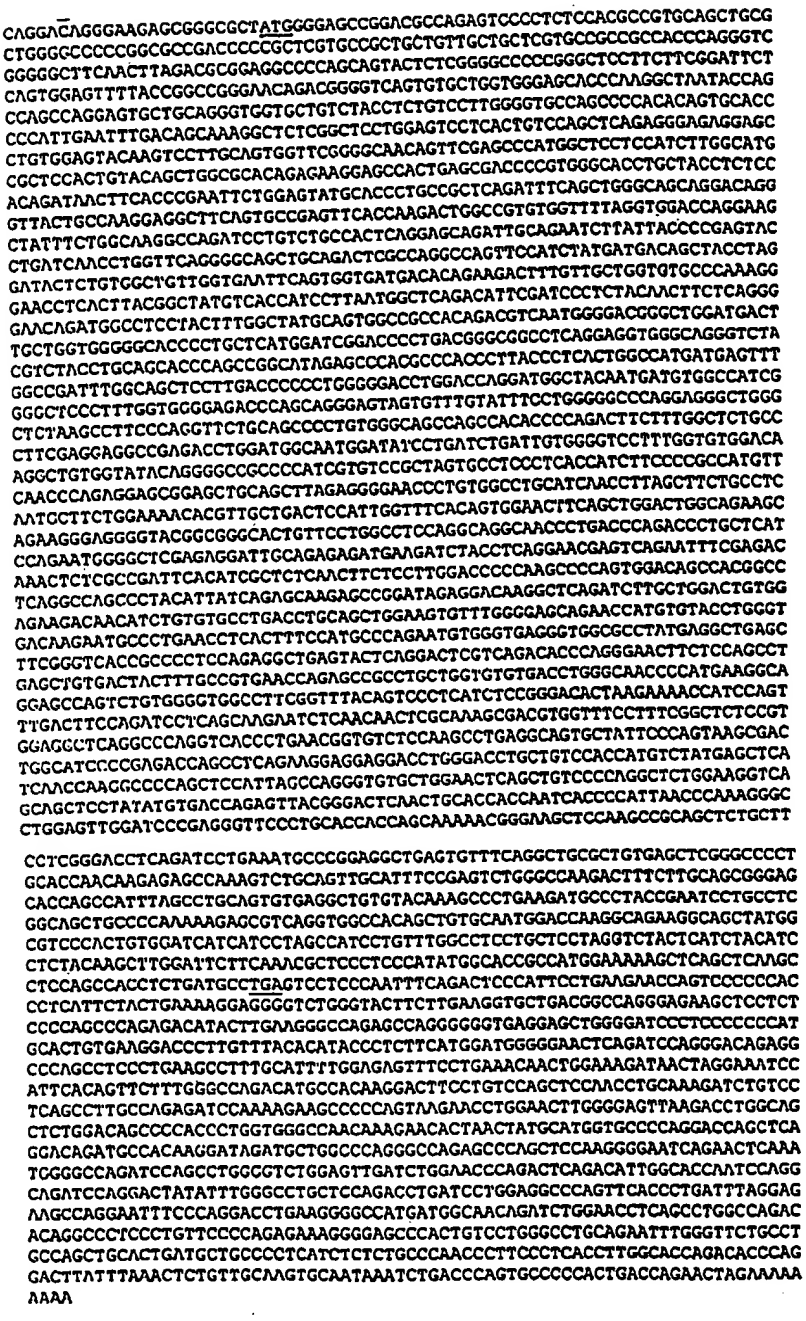

FIGURE 18

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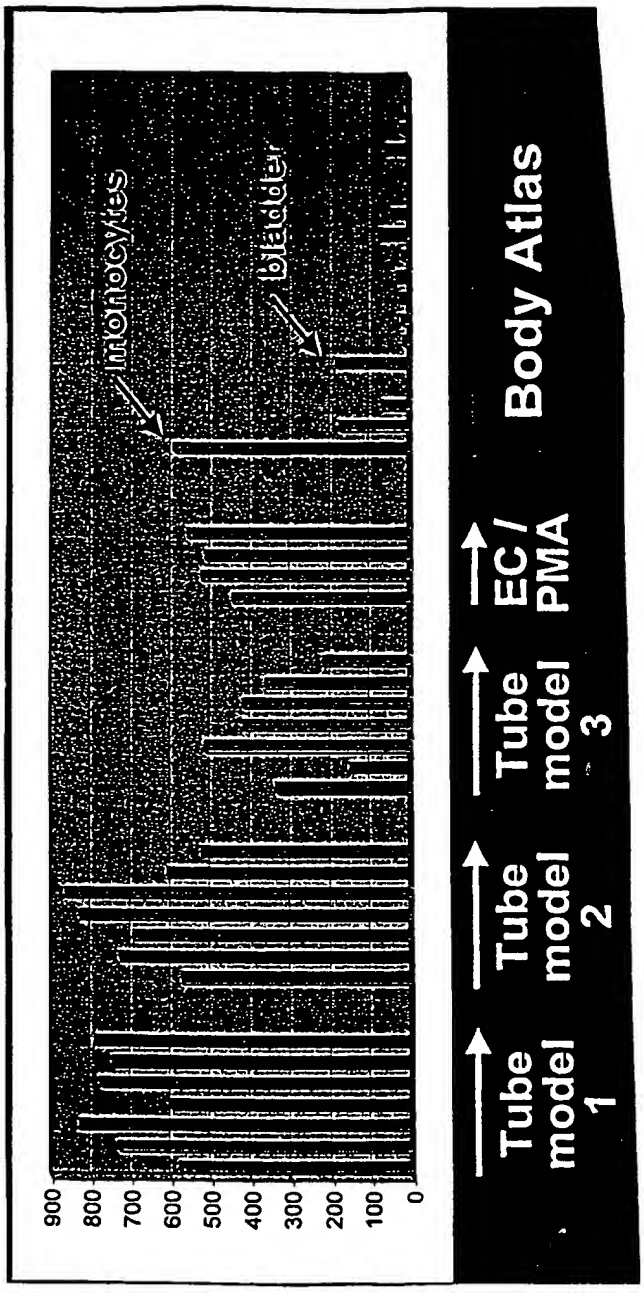
ELDPEGSLHHQQKRFAPSRSSASSGPQILKCPEAECFRLRCELGPLHQQESQSLQLHFRVWAKTFLQREHQPFSLQCEAV
YKALKMPYRILPRQLPQKERQVATAVQWTKAEGSYGVPLWIIILAILFGLLLGLLIYILYKLGFFKRSLPYGTAMEKAQ
LKPPATSDA

FIGURE 19


Monocytes
bladder
900
800
700
600
500
400
300
200
100
0
Tube model 1
Tube model 2
Tube model 3
EC / PMA
Body Atlas

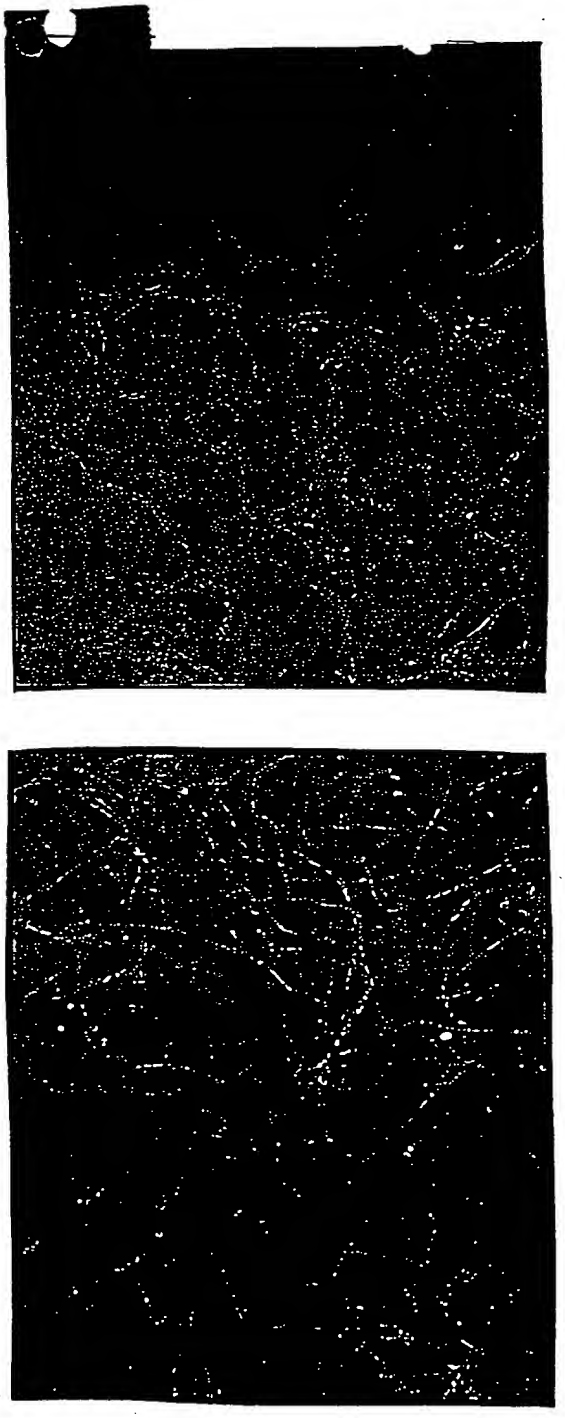


FIGURE 20

AAA9 cDNA Sequence

AAGGCCCTGCCAGCTTGGGAGGGAATTGTCCCTGCCTGCTTCTGGAGAAAGAAGATATTGACACCATCTAC
GGGCACCGAAGGAACTGCTTCAAGTGACCATTCTTTTTCTTCTGCCCAGTATTTGCAGCAGTAACAGCACAG
GTGTTTTAGAGGCAGCTAATAATTCACTTGTTGTTACTACAACAAAACCATCTATAACAACACCAAACACA
GAATCATTACAGAAAAATGTTGTCACACCAACAACTGGAACAACTCCTAAAGGAACAATCACCAATGAATT
ACTTAAAATGTCTCTGATGTCAACAGCTACTTTTTTAACAAGTAAAGATGAAGGATTGAAAGCCACAACCA
CTGATGTCAGGAAGAATGACTCCATCATTTCAAACGTAACAGTAACAAGTGTTACACTTCCCAATGCTGTT
TCAACATTACAAAGTTCCAAACCCAAGACTGAAACTCAGAGTTCAATTAAAACAACAGAAATACCAGGTAG
TGTTCTACAACCAGATGCATCACCTTCTAAAACTGGTACATTAACCTCAATACCAGTTACAATTCCAGAAA
ACACCTCACAGTCTCAAGTAATAGRCACTGAGGGTGGAAAAAATGCAAGCACTTCAGCAACCAGCCGGTCT
TATTCCAGTATTATTTTGCCGGTGGTTATTGCTTTGATTGTAATAACACTTTCAGTATTTGTTCTGGTGGG
TTTGTACCGAATGTGCTGGAAGGCAGATCCGGGCACACCAGAAAATGGAAATGATCAACCTCAGTCTGATA
AAGAGAGCGTGAAGCTTCTTACCGTTAAGACAATTTCTCATGAGTCTGGTGAGCACTCTGCACAAGGAAAA
ACCAAGAACTGGCAGCTTGAGGAATTCTCTCCACACCTAGGCAATAATTACGCTTAATCTTCAGCTTCTAT
GCACCAAGCGTGGAAAAGGAGAAAGTCCTGCAGAATCAATCCCGACTTCCATACCTGCTGCTGGACTGTAC
CAGACGTCTGTCCCAGTAAAGTGATGTCCAGCTGACATGCAATAATTTGATGGAATCAAAAAGAACCCCGG
GGCTCTCCTGTTCTCTCACATTTAAAAATTCCATTACTCCATTTACAGGAGCGTTCCTAGGAAAAGGAATT
TTAGGAGGAGAATTTGTGAGCAGTGAATCTGACAGCCCAGGAGGTGGGCTCGCTGATAGGCATGACTTTCC
TTAATGTTTAAAGTTTTCCGGGCCAAGAATTTTTATCCATGAAGACTTTCCTACTTTTCTCGGTGTTCTTA
TATTACCTACTGTTAGTATTTATTGTTTACCACTATGTTAATGCAGGGAAAAGTTGCACGTGTATTATTAA
ATATTAGGTAGAAATCATACCATGCTACTTTGTACATATAAGTATTTTATTCCTGCTTTCGTGTTACTTTT
AATAAATAACTACTGTACTCAATACTCTAAAAATACTATAACATGACTGTGAAAATGGCAATGTTATTGTC
TTCCTATAATTATGAATATTTTTGGATGGATTATTAGAATACATGAACTCACTAATGAAAGGCATTTGTAA
TAAGTCAGAAAGGGACATAGGATTCACATATCAGACTGTTAGGGGGAGAGNTAATTATCAGTTCTTTGGTC
TTTCTATTTGTCATTCATACTATGTGATGAAGATGTAAGTGCAAGGGCATTTATAACACTATACTGCATTC
ATTAGATAT

FIGURE 21

AAA9 Protein

MELLQYTILFLLPSICSSNSTGVLEAANNSLVVTTTKPSITTPNTESLQKNVVTPTTGTTPKGTITNELLK
MSLMSTATFLTSKDEGLKATTTDVRKNDSIISNVTVTSVTLPNAVSTLQSSKPKTETQSSIKTTEIPGSVL
QPDASPSKTGTLTSIPVTIPENTSQSQVIXTEGGKNASTSATSRSYSSIILP[redacted]Y
RMCWKADPGTPENGNDQPQSDKESVKLLTVKTISHESGEHSAQGKTKN

FIGURE 22

AAB4 (MMP10)

ATCATCTTGCATTCCTTGTGCTGTTGTGTCTGCCAGTCTGCTCTGCCTATCCTCTGAGTGGGG
CAGCAAAAGAGGAGGACTCCAACAAGGATCTTGCCCAGCAATACCTAGAAAAGTACTACAAC
CTCGAAAAGGATGTGAAACAGTTTAGAAGAAAGGACAGTAATCTCATTGTTAAAAAAATCCA
AGGAATGCAGAAGTTCCTTGGGTTGGAGGTGACAGGGAAGCTAGACACTGACACTCTGGAGG
TGATGCGCAAGCCCAGGTGTGGAGTTCCTGACGTTGGTCACTTCAGCTCCTTTCCTGGCATGCC
GAAGTGGAGGAAAACCCACCTTACATACAGGATTGTGAATTATACACCAGATTTGCCAAGAG
ATGCTGTTGATTCTGCCATTGAGAAAGCTCTGAAAGTCTGGGAAGAGGTGACTCCACTCACAT
TCTCCAGGCTGTATGAAGGAGAGGCTGATATAATGATCTCTTTCGCAGTTAAAGAACATGGAG
ACTTTTACTCTTTTGATGGCCCAGGACACAGTTTGGCTCATGCCTACCCACCTGGACCTGGGCT
TTATGGAGATATTCACTTTGATGATGATGAAAAATGGACAGAAGATGCATCAGGCACCAATTT
ATTCCTCGTTGCTGCTCATGAACTTGGCCACTCCCTGGGGCTCTTTCACTCAGCCAACACTGAA
GCTTTGATGTACCCACTCTACAACTCATTCACAGAGCTCGCCCAGTTCCGCCTTTCGCAAGATG
ATGTGAATGGCATTCAGTCTCTCTACGGACCTCCCCCTGCCTCTACTGAGGAACCCCTGGTGCC
CACAAAATCTGTTCCTTCGGGATCTGAGATGCCAGCCAAGTGTGATCCTGCTTTGTCCTTCGAT
GCCATCAGCACTCTGAGGGGAGAATATCTGTTCTTTAAAGACAGATATTTTTGGCGAAGATCC
CACTGGAACCCTGAACCTGAATTTCATTTGATTTCTGCATTTTGGCCCTCTCTTCCATCATATTT
GGATGCTGCATATGAAGTTAACAGCAGGGACACCGTTTTTATTTTTAAAGGAAATGAGTTCTG
GGCCATCAGAGGAAATGAGGTACAAGCAGGTTATCCAAGAGGCATCCATACCCTGGGTTTTC
CTCCAACCATAAGGAAAATTGATGCAGCTGTTTCTGACAAGGAAAAGAAGAAAACATACTTC
TTTGCAGCGGACAAATACTGGAGATTTGATGAAAATAGCCAGTCCATGGAGCAAGGCTTCCCT
AGACTAATAGCTGATGACTTTCCAGGAGTTGAGCCTAAGGTTGATGCTGTATTACAGGCATTT
GGATTTTTCTACTTCTTCAGTGGATCATCACAGTTTGAGTTTGACCCCAATGCCAGGATGGTGA
CACACATATTAAAGAGTAACAGCTGGTTACATTGCTCTAGA[redacted]

FIGURE 23

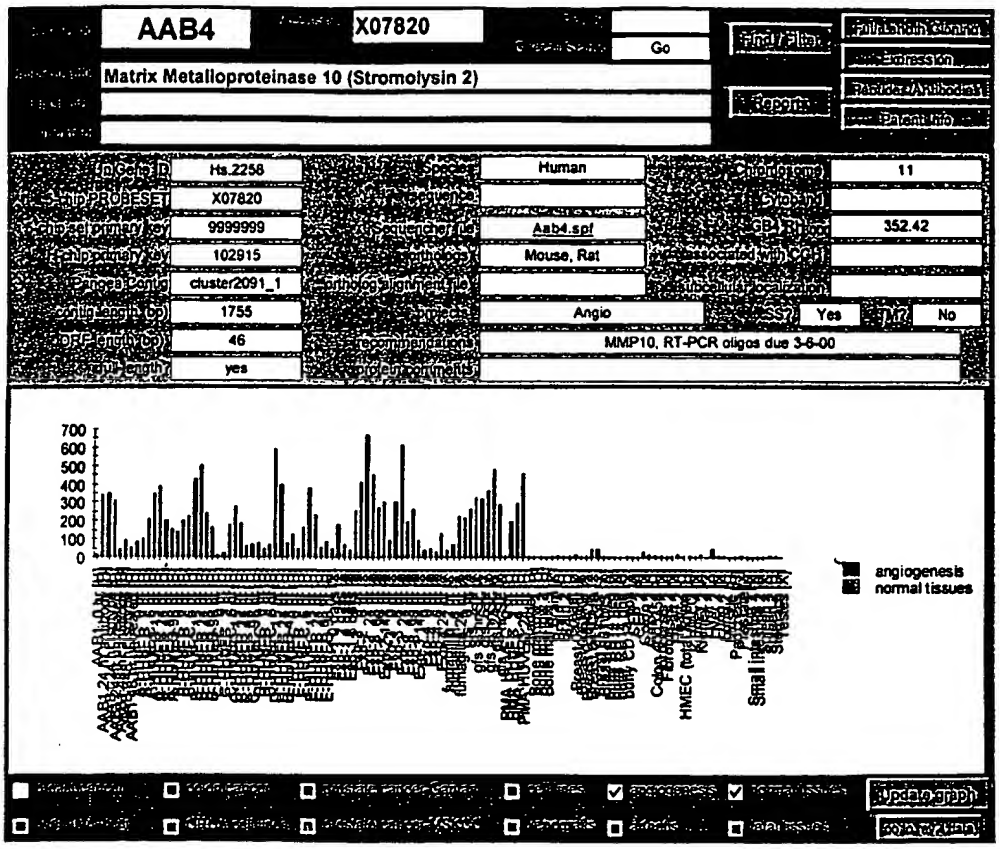

AAB4
X07820
Go
Find / Filter
Export
Matrix Metalloproteinase 10 (Stromolysin 2)
Hs.2258
Human
11
X07820
352.42
9999999
Aab4.spf
102915
Mouse, Rat
cluster2091_1
1755
Angio
Yes
No
46
MMP10, RT-PCR oligos due 3-6-00
yes
700
600
500
400
300
200
100
0
angiogenesis
normal tissues
Update graph

FIGURE 24

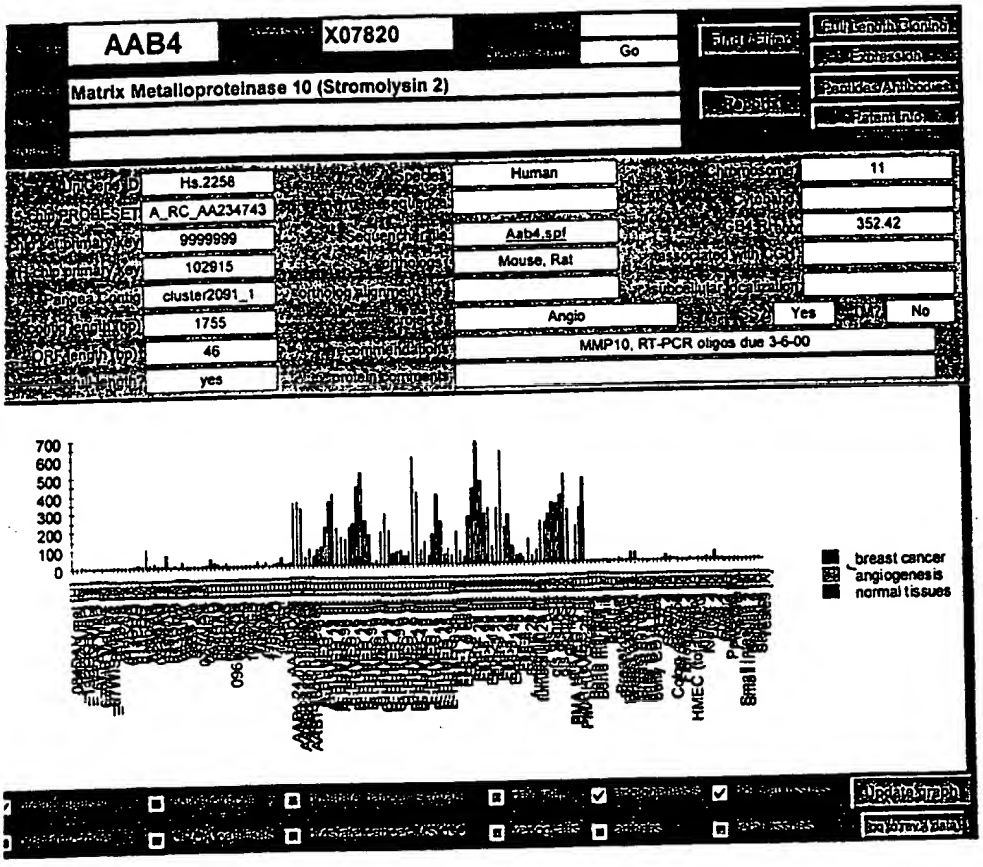

AAB4
X07820
Go
Matrix Metalloproteinase 10 (Stromolysin 2)
Hs.2258
A_RC_AA234743
9999999
102915
cluster2091_1
1755
46
yes
Human
Aab4.spf
Mouse, Rat
Angio
Yes
No
MMP10, RT-PCR oligos due 3-6-00
11
352.42
700
600
500
400
300
200
100
0
breast cancer
angiogenesis
normal tissues

FIGURE 25